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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

15 In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

20 In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84 % amino acid sequence identity, alternatively at least about 85 % amino acid sequence identity, alternatively at least about 86 % amino acid sequence identity, alternatively at least about 87 % amino acid sequence identity, alternatively at least about 88 % amino acid sequence identity, alternatively at least about 89 % amino acid sequence identity, alternatively at least about 90 % amino acid sequence identity, alternatively at least about 91 % amino acid sequence identity, alternatively at least about 92 % amino acid sequence identity, alternatively at least about 93 % amino acid sequence identity, alternatively at least about 94 % amino acid sequence identity, alternatively at least about 95 % amino acid sequence identity, alternatively at least about 96 % amino acid sequence identity, alternatively at least about 97 % amino acid sequence identity, alternatively at least about 98 % amino acid sequence identity and alternatively at least about 99 % amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1B show a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO6004 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA92259".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figures 1A-1B.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO4981 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA94849-2960".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO7174 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA96883-2745".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO5778 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA96894-2675".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4332 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA100272-2969".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO9799 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA108696-2966".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO9909 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA117935-2801".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO9917 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA119474-2803".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO9771 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA119498-2965".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO9877 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA119502-2789".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO9903 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA119516-2797".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO9830 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA119530-2968".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO7155 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA121772-2741".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO9862 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA125148-2782".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO9882 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA125150-2793".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO9864 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA125151-2784".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO10013 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA125181-2804".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO9885 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA125192-2794".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO9879 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA125196-2792".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO10111 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA125200-2810".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO9925 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA125214-2814".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO9905 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA125219-2799".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO10276 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA128309-2825".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO9898 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA129535-2796".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO9904 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA129549-2798".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO19632 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA129580-2863".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO19672 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA129794-2967".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO9783 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA131590-2962".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO10112 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA135173-2811".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figures 59A-59B show a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO10284 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA138039-2828".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figures 59A-59B.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO10100 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA139540-2807".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO19628 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA139602-2859".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO19684 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA139632-2880".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO10274 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA139686-2823".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO9907 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA142392-2800".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO9873 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA143076-2787".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO10201 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA143294-2818".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO10200 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA143514-2817".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO10196 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA144841-2816".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO10282 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA148380-2827".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO19650 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA149995-2871".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO21184 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA167678-2963".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO21201 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA168028-2956".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO21175 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA173894-2947".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO21340 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA176775-2957".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO21384 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA177313-2982".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO982 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA57700-1408".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO1160 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA62872-1509".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1187 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA62876-1517".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA66660-1585".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO231 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA34434-1139".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO357 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA44804-1248".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO725 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA52758-1399".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA59849-1504".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1306 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA65410-1569".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA71290-1630".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO229 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA33100-1159".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1272 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA64896-1539".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4405 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84920-2614".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO181 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA23330-1390".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO214 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA32286-1191".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO247 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA35673-1201".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO337 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA43316-1237".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO526 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA44184-1319".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO363 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA45419-1252".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO531 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA48314-1320".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA50921-1458".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO840 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA53987".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56047-1456".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO788 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56405-1357".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56531-1648".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56865-1491".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO826 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA57694-1341".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1005 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA57708-1411".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO809 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA57836-1338".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA57841-1522".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA58847-1383".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA59212-1627".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA59588-1571".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1025 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA59622-1334".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA59847-2510".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA60615-1483".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA60621-1516".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA62814-1521".

10 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1244 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA64883-1526".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA64889-1541".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1412 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA64897-1628".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA64903-1553".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1330 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA64907-1163-1".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1347 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA64950-1590".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA64952-1568".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA65402-1540".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA65405-1547".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1340 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA66663-1598".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA66667".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA66675-1587".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1376 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA67300-1605".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA68872-1620".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA71269-1621".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1488 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA73736-1657".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA73739-1645".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA76400-2528".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA76532-1702".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA76541-1675".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA79862-2522".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA81754-2532".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA81761-2583".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO5723 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA82361".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA83500-2506".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA84210-2576".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO3543 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA86571-2551".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO3444 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA87997".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA92218-2554".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA92223-2567".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO5725 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA92265-2669".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO4408 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA92274-2617".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO9940 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA92282".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO7154 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA108760-2740".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO7425 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA108792-2753".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA111750-2706".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO9836 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA119514-2772".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA125185-2806".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

15 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein
20 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing,
25 treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*,
30 an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in
35 bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino

acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

5 The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1 % of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5 % of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

10 The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

20 "PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid

sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

5 "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed
 10 herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid
 15 sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95%
 20 nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or
 25 without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180
 30 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences
 35 identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent

nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against

which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated

polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still

capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H - V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA₁, and IgA₂.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing

conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

5 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

10 By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a
15 discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

20 A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
5  * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10 int _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

40

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX           4      /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
15
#define DINS1         1      /* penalty per base */
#define PINS0         8      /* penalty for a gap */
#define PINS1         4      /* penalty per residue */

struct jmp {
20
    short            n[MAXJMP];    /* size of jmp (neg for dely) */
    unsigned short   x[MAXJMP];    /* base no. of jmp in seq x */
};                                /* limits seq to 2^16 -1 */

struct diag {
25
    int              score;         /* score at last jmp */
    long             offset;        /* offset of prev block */
    short            jmp;           /* current jmp index */
    struct jmp        jp;           /* list of jmps */
};

30
struct path {
    int              spc;           /* number of leading spaces */
    short            n[JMPs];       /* size of jmp (gap) */
    int              x[JMPs];       /* loc of jmp (last elem before gap) */
35
};

char              *ofile;          /* output file name */
char              *namex[2];       /* seq names: getseqs() */
char              *prog;           /* prog name for err msgs */
40
char              *seqx[2];        /* seqs: getseqs() */
int               dmax;            /* best diag: nw() */
int               dmax0;          /* final diag */
int               dna;            /* set if dna: main() */
int               endgaps;        /* set if penalizing end gaps */
45
int               gapx, gapy;      /* total gaps in seqs */
int               len0, len1;      /* seq lens */
int               ngapx, ngapy;    /* total size of gaps */
int               smax;           /* max score: nw() */
int               *xbm;           /* bitmap for matching */
50
long              offset;         /* current offset in jmp file */
struct            diag            *dx;    /* holds diagonals */
struct            path            pp[2];  /* holds path for seqs */

char              *calloc(), *malloc(), *index(), *strcpy();
55
char              *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5 * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
15 #include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
20 };

static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
25    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                main
30     int      ac;
     char      *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
         fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
         fprintf(stderr, "The sequences can be in upper- or lower-case\n");
         fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
         fprintf(stderr, "Output is in the file \"align.out\"\n");
         exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                                /* 1 to penalize endgaps */
    ofile = "align.out";                        /* output file */

50     nw();                                /* fill in the matrix, get the possible jumps */
    readjumps();                                /* get the actual jumps */
    print();                                /* print stats, alignment */

55     cleanup(0);                            /* unlink any tmp files */
}

```

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
5  * When scores are equal, we prefer mismatches to any gap, prefer
   * a new gap to extending an ongoing gap, and prefer a gap in seqx
   * to a gap in seq y.
   */
nw()
{
10     char *      *px, *py;          /* seqs and prs */
    int          *ndely, *dely;      /* keep track of dely */
    int          ndelx, delx;        /* keep track of delx */
    int          *tmp;               /* for swapping row0, row1 */
    int          mis;                /* score for each type */
15     int          ins0, ins1;        /* insertion penalties */
    register     id;                 /* diagonal index */
    register     ij;                 /* jmp index */
    register     *col0, *col1;       /* score for curr, last row */
    register     xx, yy;              /* index into seqs */
20
    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
25     col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

30     smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
35         }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
40         dely[yy] = -ins0;

    /* fill in match matrix
    */
45     for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
50                 col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
55             col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
60

```


Table 1 (cont')

...nw

```

5      for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

10      /* update penalty for del in x seq;
        * favor new del over ongoing del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
15            if (col0[yy] - ins0 >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
20            }
        } else {
            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
25            } else
                ndely[yy]++;
        }

        /* update penalty for del in y seq;
        * favor new del over ongoing del
        */
        if (endgaps || ndelx < MAXGAP) {
30            if (col1[yy-1] - ins0 >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
35            } else {
                delx -= ins1;
                ndelx++;
            }
        } else {
40            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else
45                ndelx++;
        }

        /* pick the maximum score; we're favoring
50        * mis over any del and delx over dely
        */

```

55

60

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
5   else if (delx >= dely[yy]) {
        coll[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
15      offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
    else {
        coll[yy] = dely[yy];
        ij = dx[id].ijmp;
25   if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
30      offset += sizeof(struct jmp) + sizeof(offset);
            }
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
    }
    if (xx == len0 && yy < len1) {
40      /* last col
        */
        if (endgaps)
            coll[yy] -= ins0+ins1*(len1-yy);
        if (coll[yy] > smax) {
45      smax = coll[yy];
            dmax = id;
        }
    }
}
50   if (endgaps && xx < len0)
        coll[yy-1] -= ins0+ins1*(len0-xx);
    if (coll[yy-1] > smax) {
        smax = coll[yy-1];
        dmax = id;
55   }
    tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
60   (void) free((char *)col0);
    (void) free((char *)coll);
}

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3 /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print() print
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
50     }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
55     }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int    lx, ly;          /* "core" (minus endgaps) */
    int    firstgap, lastgap; /* leading trailing overlap */
{
    int    nm, i0, i1, siz0, siz1;
10    char    outx[32];
    double    pct;
    register    n0, n1;
    register char    *p0, *p1;

15    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25         if (siz0) {
             p1++;
             n1++;
             siz0--;
         }
30         else if (siz1) {
             p0++;
             n0++;
             siz1--;
         }
35         else {
             if (xbm[*p0-'A']&xbm[*p1-'A'])
                 nm++;
             if (n0++ == pp[0].x[i0])
                 siz0 = pp[0].n[i0++];
40             if (n1++ == pp[1].x[i1])
                 siz1 = pp[1].n[i1++];
             p0++;
             p1++;
         }
45     }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

Table 1 (cont')

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "": "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINSO, PINS1);
    if (endgaps)
        fprintf(fx,
            "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
    else
        fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nm = stripname(name[i]);
        if (nm > lmax)
            lmax = nm;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25            po[i]++;
            ps[i]++;

            /*
30            * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
35                * we need to merge all gaps
                * at this location
                */
                siz[i] = pp[i].n[ij[i] + +];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + +];
40            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
45        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
50 }

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

```

...pr_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10             putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15         }
    }
}

```

```

20  /*
    * put out a number line: dumpblock()
    */

```

```

static
nums(ix)

```

nums

```

25  {
    int      ix;      /* index in out[] holding seq line */

    char      nline[P_LINE];
    register  i, j;
    register char *pn, *px, *py;

30      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
          if (*py == ' ' || *py == '-')
              *pn = ' ';
35          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
                  for (px = pn; j; j /= 10, px--)
                      *px = j%10 + '0';
40                  if (i < 0)
                      *px = '-';

                  }
              else
45                  *pn = ' ';
                  i++;
          }
      }
      *pn = '\0';
      nc[ix] = i;
50      for (pn = nline; *pn; pn++)
          (void) putc(*pn, fx);
      (void) putc('\n', fx);
}

```

```

55  /*
    * put out a line (name, [num], seq, [num]): dumpblock()
    */

```

```

static
putline(ix)

```

putline

```

60      int      ix;      {

```

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i; i--)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {
40             if (xbm[*p0-'A'] & xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

60

```

stars

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
20 }

```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>
10 char    *jname = "/tmp/homgXXXXXX";      /* tmp file for jumps */
FILE      *fj;

int        cleanup();                      /* cleanup tmp file */
15 long     lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                                cleanup
    int      i;
{
    if (fj)
        (void) unlink(jname);
25     exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char      *
getseq(file, len)                                getseq
35     char    *file;      /* file name */
     int      *len;       /* seq len */
{
     char      line[1024], *pseq;
     register char *px, *py;
     int      natgc, tlen;
     FILE      *fp;

     if ((fp = fopen(file, "r")) == 0) {
         fprintf(stderr, "%s: can't read %s\n", prog, file);
45         exit(1);
     }
     tlen = natgc = 0;
     while (fgets(line, 1024, fp)) {
         if (*line == ';' || *line == '<' || *line == '>')
50             continue;
         for (px = line; *px != '\n'; px++)
             if (isupper(*px) || islower(*px))
                 tlen++;
     }
55     if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
         fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
         exit(1);
     }
     pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);

5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
15
    }
}
*py++ = '\0';
*py = '\0';
20
(void) fclose(fp);
dna = natgc > (tlen/3);
return(pseq+4);
}

25
char *
g_alloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
30
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35
            fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

40
/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
45
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50
    if (f) {
        (void) fclose(f);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
60
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

g_alloc

readjmps

Table 1 (cont')**...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
10    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
             */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
40    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
60    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
25
30
35
40
45
50
55
60

```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
15 Comparison Protein	XXXXXXXXYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20 (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Table 4

25

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein
20 as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the
25 nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

30 In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35 Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

 Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

5 Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1
10 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl
15 esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.
25

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.
30

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding
35

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* 15 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not 20 limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant 25 cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, 30 ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, 10 penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as 15 signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for 20 cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); 30 Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well 35 known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

5 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

10 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

15 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

20 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

25 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

30 Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for

a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means.

The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection,

electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based

assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos: 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective

genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically

acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single

Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

5 The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

10 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

15 The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

20 In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

35 If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers

(Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are

prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251: 1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

15 F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate
25 the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an
35 immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally,

either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal

antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences

of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

5 Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of
10 human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10
20 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding
25 specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of
30 the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

35 Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the

first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar
10 size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

 Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical
15 linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives
20 is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

 Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized
25 bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

 Various technique for making and isolating bispecific antibody fragments directly from recombinant cell
30 culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by
35 Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on

the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol., 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared.

5 Tutt *et al.*, J. Immunol., 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms
10 to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

15 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using
20 known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

25 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176:
30 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.*, Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design,
35 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

5 If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, 10 *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in 15 amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques 20 are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in 25 the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. 30 While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered 35 to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2 x 10⁶ cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1 x 10⁷ cells/ml (approx. OD₆₀₀=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μ g, vol. < 10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l Klentaq (Clontech, Palo Alto, CA); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:245)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:246)

PCR was then performed as follows:

- | | | | |
|----|----|--------------|------------------|
| 35 | a. | Denature | 92°C, 5 minutes |
| | b. | 3 cycles of: | |
| | | Denature | 92°C, 30 seconds |
| | | Anneal | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA94849-2960	PTA-2306	July 25, 2000
	DNA96883-2745	PTA-544	August 17, 1999
5	DNA96894-2675	PTA-260	June 22, 1999
	DNA100272-2969	PTA-2299	July 25, 2000
	DNA108696-2966	PTA-2315	August 1, 2000
	DNA117935-2801	PTA-1088	December 22, 1999
	DNA119474-2803	PTA-1097	December 22, 1999
10	DNA119498-2965	PTA-2298	July 25, 2000
	DNA119502-2789	PTA-1082	December 22, 1999
	DNA119516-2797	PTA-1083	December 22, 1999
	DNA119530-2968	PTA-2396	August 8, 2000
	DNA121772-2741	PTA-1030	December 7, 1999
15	DNA125148-2782	PTA-955	November 16, 1999
	DNA125150-2793	PTA-1085	December 22, 1999
	DNA125151-2784	PTA-1029	December 7, 1999
	DNA125181-2804	PTA-1096	December 22, 1999
	DNA125192-2794	PTA-1086	December 22, 1999
20	DNA125196-2792	PTA-1091	December 22, 1999
	DNA125200-2810	PTA-1186	January 11, 2000
	DNA125214-2814	PTA-1270	February 2, 2000
	DNA125219-2799	PTA-1084	December 22, 1999
	DNA128309-2825	PTA-1340	February 8, 2000
25	DNA129535-2796	PTA-1087	December 22, 1999
	DNA129549-2798	PTA-1099	December 22, 1999
	DNA129580-2863	PTA-1584	March 28, 2000
	DNA129794-2967	PTA-2305	July 25, 2000
	DNA131590-2962	PTA-2297	July 25, 2000
30	DNA135173-2811	PTA-1184	January 11, 2000
	DNA138039-2828	PTA-1343	February 8, 2000
	DNA139540-2807	PTA-1187	January 11, 2000
	DNA139602-2859	PTA-1588	March 28, 2000
	DNA139632-2880	PTA-1629	April 4, 2000
35	DNA139686-2823	PTA-1264	February 2, 2000
	DNA142392-2800	PTA-1092	December 22, 1999
	DNA143076-2787	PTA-1028	December 7, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA143294-2818	PTA-1182	January 11, 2000
	DNA143514-2817	PTA-1266	February 2, 2000
	DNA144841-2816	PTA-1188	January 11, 2000
5	DNA148380-2827	PTA-1181	January 11, 2000
	DNA149995-2871	PTA-1971	May 31, 2000
	DNA167678-2963	PTA-2302	July 25, 2000
	DNA168028-2956	PTA-2304	July 25, 2000
	DNA173894-2947	PTA-2108	June 20, 2000
10	DNA176775-2957	PTA-2303	July 25, 2000
	DNA177313-2982	PTA-2251	July 19, 2000
	DNA57700-1408	203583	January 12, 1999
	DNA62872-1509	203100	August 4, 1998
	DNA62876-1517	203095	August 4, 1998
15	DNA66660-1585	203279	September 22, 1998
	DNA34434-1139	209252	September 16, 1997
	DNA44804-1248	209527	December 10, 1997
	DNA52758-1399	209773	April 14, 1998
	DNA59849-1504	209986	June 16, 1998
20	DNA65410-1569	203231	September 15, 1998
	DNA71290-1630	203275	September 22, 1998
	DNA33100-1159	209377	October 16, 1997
	DNA64896-1539	203238	September 9, 1998
	DNA84920-2614	203966	April 27, 1999
25	DNA23330-1390	209775	April 14, 1998
	DNA32286-1191	209385	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA43316-1237	209487	November 21, 1997
	DNA44184-1319	209704	March 26, 1998
30	DNA45419-1252	209616	February 5, 1998
	DNA48314-1320	209702	March 26, 1998
	DNA50921-1458	209859	May 12, 1998
	DNA53987	209858	May 12, 1998
	DNA56047-1456	209948	June 9, 1998
35	DNA56405-1357	209849	May 6, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	DNA57694-1341	203017	June 23, 1998
	DNA57708-1411	203021	June 23, 1998
	DNA57836-1338	203025	June 23, 1998
	DNA57841-1522	203458	November 3, 1998
5	DNA58847-1383	209879	May 20, 1998
	DNA59212-1627	203245	September 9, 1998
	DNA59588-1571	203106	August 11, 1998
	DNA59622-1334	209984	June 16, 1998
	DNA59847-2510	203576	January 12, 1999
10	DNA60615-1483	209980	June 16, 1998
	DNA60621-1516	203091	August 4, 1998
	DNA62814-1521	203093	August 4, 1998
	DNA64883-1526	203253	September 9, 1998
	DNA64889-1541	203250	September 9, 1998
15	DNA64897-1628	203216	September 15, 1998
	DNA64903-1553	203223	September 15, 1998
	DNA64907-1163-1	203242	September 9, 1998
	DNA64950-1590	203224	September 15, 1998
	DNA64952-1568	203222	September 15, 1998
20	DNA65402-1540	203252	September 9, 1998
	DNA65405-1547	203476	November 17, 1998
	DNA66663-1598	203268	September 22, 1998
	DNA66667	203267	September 22, 1998
	DNA66675-1587	203282	September 22, 1998
25	DNA67300-1605	203163	August 25, 1998
	DNA68872-1620	203160	August 25, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA73736-1657	203466	November 17, 1998
	DNA73739-1645	203270	September 22, 1998
30	DNA76400-2528	203573	January 12, 1999
	DNA76532-1702	203473	November 17, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA79862-2522	203550	December 22, 1998
	DNA81754-2532	203542	December 15, 1998
35	DNA81761-2583	203862	March 23, 1999
	DNA83500-2506	203391	October 29, 1998
	DNA84210-2576	203818	March 2, 1999

Table 7 (cont')

	DNA86571-2551	203660	February 9, 1999
	DNA92218-2554	203834	March 9, 1999
	DNA92223-2567	203851	March 16, 1999
	DNA92265-2669	PTA-256	June 22, 1999
5	DNA92274-2617	203971	April 27, 1999
	DNA108760-2740	PTA-548	August 17, 1999
	DNA108792-2753	PTA-617	August 31, 1999
	DNA111750-2706	PTA-489	August 3, 1999
	DNA119514-2772	PTA-946	November 9, 1999
10	DNA125185-2806	PTA-1031	December 7, 1999

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

EXAMPLE 5: Isolation of cDNA clones Encoding Human PRO6004, PRO5723, PRO3444, and PRO9940

DNA molecules encoding the PRO840, PRO1338, PRO6004, PRO5723, PRO3444, and PRO9940 polypeptides shown in the accompanying figures were obtained through GenBank.

EXAMPLE 6: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following

high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 7: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g

Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

5 *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

15 The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

25 Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in mammalian cells

35 This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector.

Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

5 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

15 Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ^{35}S -cysteine and 200 μ Ci/ml ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

20 In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompariyac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris.

25 The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

30 In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

35 Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells

can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

5 Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

10 Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits
15 selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect* (Qiagen), Dosper* or Fugene* (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

20 The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media ($0.2 \mu\text{m}$ filtered PS20 with 5% $0.2 \mu\text{m}$ diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C . After another 2-3 days, 250 mL, 500 mL and 2000
25 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is
30 sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C , and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a $0.22 \mu\text{m}$ filter. The filtrate was either stored at 4°C or immediately
35 loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is

pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

5 Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently
10 desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Yeast

15 The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal
20 peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with
25 Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

30

EXAMPLE 10: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG).
35 A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding

the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 11: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with

additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 12: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration

of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 13: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 14: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson,

Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 15: Pericyte c-Fos Induction (Assay 93)

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 μ l of PRO polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

The following polypeptides tested positive in this assay: PRO982, PRO1160, PRO1187, and PRO1329.

EXAMPLE 16: Chondrocyte Re-differentiation Assay (Assay 110)

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO357.

EXAMPLE 17: Identification of PRO Polypeptides That Stimulate TNF-α Release In Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF-α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF-α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF-α release would be beneficial. Specifically, 200 µl of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300µl of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50µl of plasma is collected from each well and tested for the presence of TNF-α by ELISA assay. A positive in the assay is a higher amount of TNF-α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay: PRO231, PRO357, PRO725, PRO1155, PRO1306, and PRO1419.

EXAMPLE 18: Promotion of Chondrocyte Redifferentiation (Assay 129)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control)

or the test PRO polypeptide are added to give a final volume of 200 μ l/well. After 5 days at 37°C, 22 μ l of media containing 100 μ g/ml Hoechst 33342 and 50 μ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

The following PRO polypeptides tested positive in this assay: PRO229, PRO1272, and PRO4405.

EXAMPLE 19: Normal Human Dermal Fibroblast Proliferation (Assay 141)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce proliferation of human dermal fibroblast cells in culture and, therefore, function as useful growth factors.

On day 0, human dermal fibroblast cells (from cell lines, maximum of 12-14 passages) were plated in 96-well plates at 1000 cells/well per 100 microliter and incubated overnight in complete media [fibroblast growth media (FGM, Clonetics), plus supplements: insulin, human epithelial growth factor (hEGF), gentamicin (GA-1000), and fetal bovine serum (FBS, Clonetics)]. On day 1, complete media was replaced by basal media [FGM plus 1% FBS] and addition of PRO polypeptides at 1%, 0.1% and 0.01%. On day 7, an assessment of cell proliferation was performed by Alamar Blue assay followed by Crystal Violet. Results are expressed as % of the cell growth observed with control buffer.

The following PRO polypeptides tested positive in this assay: PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 and PRO10096.

EXAMPLE 20: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes

overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from a panel of nine different tumor tissues (listed below) were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues, as compared to a non-cancerous human tissue control or other human tumor tissues. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
30	PRO6004	colon tumor	universal normal control
	PRO4981	colon tumor	universal normal control
	PRO4981	lung tumor	universal normal control
35	PRO7174	colon tumor	universal normal control
	PRO5778	lung tumor	universal normal control
	PRO5778	breast tumor	universal normal control
40	PRO5778	liver tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
	PRO4332	colon tumor	universal normal control
5	PRO9799	colon tumor	universal normal control
	PRO9909	colon tumor	universal normal control
	PRO9917	colon tumor	universal normal control
10	PRO9917	lung tumor	universal normal control
	PRO9917	breast tumor	universal normal control
	PRO9771	colon tumor	universal normal control
15	PRO9877	colon tumor	universal normal control
	PRO9903	colon tumor	universal normal control
	PRO9830	colon tumor	universal normal control
20	PRO7155	colon tumor	universal normal control
	PRO7155	lung tumor	universal normal control
	PRO7155	prostate tumor	universal normal control
25	PRO9862	colon tumor	universal normal control
	PRO9882	colon tumor	universal normal control
	PRO9864	colon tumor	universal normal control
30	PRO10013	colon tumor	universal normal control
	PRO9885	colon tumor	universal normal control
35	PRO9879	colon tumor	universal normal control
	PRO10111	colon tumor	universal normal control
	PRO10111	rectal tumor	universal normal control
40	PRO9925	breast tumor	universal normal control
	PRO9925	rectal tumor	universal normal control
	PRO9925	colon tumor	universal normal control
	PRO9925	lung tumor	universal normal control
45	PRO9905	colon tumor	universal normal control
	PRO10276	colon tumor	universal normal control
	PRO9898	colon tumor	universal normal control
50	PRO9904	colon tumor	universal normal control
	PRO19632	colon tumor	universal normal control
55	PRO19672	colon tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
5	PRO9783	colon tumor	universal normal control
	PRO9783	lung tumor	universal normal control
	PRO9783	breast tumor	universal normal control
	PRO9783	prostate tumor	universal normal control
	PRO9783	rectal tumor	universal normal control
10	PRO10112	colon tumor	universal normal control
	PRO10284	colon tumor	universal normal control
	PRO10100	colon tumor	universal normal control
15	PRO19628	colon tumor	universal normal control
	PRO19684	colon tumor	universal normal control
	PRO10274	colon tumor	universal normal control
20	PRO9907	colon tumor	universal normal control
	PRO9873	colon tumor	universal normal control
	PRO10201	colon tumor	universal normal control
25	PRO10200	colon tumor	universal normal control
	PRO10196	colon tumor	universal normal control
	PRO10282	lung tumor	universal normal control
30	PRO10282	breast tumor	universal normal control
	PRO10282	colon tumor	universal normal control
	PRO10282	rectal tumor	universal normal control
	PRO10282	rectal tumor	universal normal control
35	PRO19650	colon tumor	universal normal control
	PRO21184	lung tumor	universal normal control
	PRO21184	breast tumor	universal normal control
40	PRO21184	colon tumor	universal normal control
	PRO21201	breast tumor	universal normal control
	PRO21201	colon tumor	universal normal control
45	PRO21175	breast tumor	universal normal control
	PRO21175	colon tumor	universal normal control
	PRO21175	lung tumor	universal normal control
50	PRO21340	colon tumor	universal normal control
	PRO21340	prostate tumor	universal normal control
	PRO21384	colon tumor	universal normal control
	PRO21384	lung tumor	universal normal control
	PRO21384	breast tumor	universal normal control

EXAMPLE 21: Tissue Expression Distribution

Oligonucleotide probes were constructed from the PRO polypeptide-encoding nucleotide sequence shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human adult and/or fetal tissue sources and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tissues tested. Knowledge of the expression pattern or the differential expression of the PRO polypeptide-encoding nucleic acid in various different human tissue types provides a diagnostic marker useful for tissue typing, with or without other tissue-specific markers, for determining the primary tissue source of a metastatic tumor, and the like. The results of these assays demonstrated the following:

(1) the DNA94849-2960 molecule is significantly expressed in the following tissues: cartilage, testis, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen aortic endothelial cells and uterus, and not significantly expressed in the following tissues: HUVEC.

(2) the DNA100272-2969 molecule is significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen and aortic endothelial cells; and not significantly expressed in uterus. Among a panel of normal and tumor cells examined, the DNA100272-2969 was found to be expressed in normal esophagus, esophageal tumor, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

(3) the DNA108696-2966 molecule is highly expressed in prostate and also expressed in testis, bone marrow and spleen. The DNA108696-2966 molecule is expressed in normal stomach, but not expressed in stomach tumor. The DNA108696-2966 molecule is not expressed in normal kidney, kidney tumor, normal lung, or lung tumor. The DNA108696-2966 molecule is highly expressed in normal rectum, lower expression in rectal tumor. The DNA108696-2966 molecule is not expressed in normal liver or liver tumor. The DNA108696-2966 molecule is not expressed in normal esophagus, esophageal tumor, cartilage, HUVEC, colon tumor, heart, placenta, adrenal gland, aortic endothelial cells and uterus.

(4) the DNA119498-2965 molecule is significantly expressed in the following tissues: highly expressed in aortic endothelial cells, and also significantly expressed in cartilage, testis, HUVEC, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate and spleen. It is not significantly expressed in uterus.

(5) the DNA119530-2968 molecule is expressed in the following tissues: normal esophagus and not expressed in the following tissues: esophageal tumors, stomach tumors, normal stomach, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumors, normal liver or liver tumors.

(6) the DNA129794-2967 molecule is significantly expressed in testis and adrenal gland; and not significantly expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, prostate, spleen, aortic endothelial cells and uterus.

(7) the DNA131590-2962 molecule is significantly expressed in the following tissues: bone marrow, adrenal

gland, prostate, spleen, uterus, cartilage, testis, colon tumor, heart, and placenta, and not significantly expressed in the following tissues: HUVEC, and aortic endothelial cells.

(8) the DNA149995-2871 molecule is highly expressed in testis, and adrenal gland; expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, prostate and uterus; weakly expressed in bone marrow, spleen and aortic endothelial cells; and not significantly expressed in placenta.

- 5 (9) the DNA167678-2963 molecule is significantly expressed in the following tissues: normal esophagus, esophagial tumor, highly expressed in normal stomach, stomach tumor, highly expressed in normal kidney, kidney tumor, expressed in lung, lung tumor, normal rectum, rectal tumor, weakly expressed in normal liver, and not significantly expressed in liver tumor.

- 10 (10) the DNA168028-2956 molecule is highly expressed in bone marrow; expressed in testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, adrenal gland, prostate, spleen, aortic endothelial cells and uterus; and is weakly expressed in cartilage. Among a panel of normal and tumor samples examined, the DNA168028-2956 was found to be expressed in stomach tumor, normal kidney, kidney tumor, lung tumor, normal rectum and rectal tumor; and not expressed in normal esophagus, esophageal tumor, normal stomach, normal lung, normal liver and liver tumor.

- 15 (11) the DNA176775-2957 molecule is highly expressed in testis; expressed in cartilage and prostate; weakly expressed in adrenal gland, spleen and uterus; and not significantly expressed in human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow and aortic endothelial cells.

- 20 (12) the DNA177313-2982 molecule is significantly expressed in prostate and aortic endothelial cells; and not significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, spleen and uterus. Among a panel of normal and tumor cells, the DNA177313-2982 molecule was found to be expressed in esophageal tumor but not in normal esophagus, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25),
5 Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).
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3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence

selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).

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4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.
6. A host cell comprising the vector of Claim 5.
7. The host cell of Claim 6, wherein said cell is a CHO cell.
8. The host cell of Claim 6, wherein said cell is an *E. coli*.
9. The host cell of Claim 6, wherein said cell is a yeast cell.
10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure

166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ

ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50
 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure
 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64),
 Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID
 NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ
 ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88
 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure
 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102),
 Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ
 ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure
 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID
 NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure
 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID
 NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure
 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID
 NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure
 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID
 NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure
 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID
 NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure
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 NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure
 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID
 NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure
 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID
 NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or
 Figure 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2
 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ
 ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18
 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure
 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32),
 Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID
 NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ
 ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56
 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure

64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ

ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80 % amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ

ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure
 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID
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 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID
 NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure
 5 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID
 NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure
 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID
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 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID
 10 NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure
 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID
 NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure
 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID
 NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure
 15 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID
 NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure
 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID
 NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure
 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID
 20 NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure
 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ
 ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID
 NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ
 25 ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26
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 30 ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64
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 Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID
 NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ
 35 ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102
 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108),
 Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure
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 10 NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure
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 NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure
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 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID
 NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ
 20 ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID
 NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ
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 NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ
 ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64
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 Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ
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 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID
 NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure

138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

20. A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO982, PRO1160, PRO1187, or PRO1329 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

20

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO357, PRO229, PRO1272 or PRO4405 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

25

22. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide, wherein the release of TNF- α from said blood is stimulated.

23. A method for stimulating the proliferation of normal human dermal fibroblast cells, said method comprising contacting said cells with a PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 or PRO10096 polypeptide, wherein the proliferation of said cells is stimulated.

35

24. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

5

25. The method of Claim 24, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, or liver tumor.

26. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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FIGURE 1A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTTGCTCGAACCAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCTGGCTGAACCGGTCAAGTATTAT
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT
GTTCAAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCTCTCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA
TTTGAAGATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCAGGAAAATGATGTGTCAATCCCAGATGTGAGGAAAAGTAAAAGTTGTTGTCAACT
TTGCTCCTACTATTCAAGGAAATTAATCTGGCACCCTGACCCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
CTTCAATGGCCCAACAAGGAATTATTATTCAAAATTTTAGCACAAAGATCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA
ACCAATGCGAGCCTGCCTCTTAACCCCTCCAAGTACAGCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTTTCTCCTGCTGCTACCTTGTGTTGACACTGTCTCTTTACCAGCATATTCT
ACCTGAAGAATGCCATTCTACAATTAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTCTGTGATAGTAAATTGCTCATTATGTAAATACTTTAAT
TCTACTCTTTTTTGATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTCAATGTTTGAATCTAC
AACTTTTCAAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCCTGTTTCAAT
AAGAGTCAATCCACATTTACAAAGATGCATTTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTGT
AAGTTCAGCATGGGTGTGCCTTCATACAATAATTTTTCTCTTGTCTCCAATAATATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACAGAGTGATCAAGTTAAACCA
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA
TGGGGTTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC
AGTATAGTAAATATAACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT
TTTCTTTTCACTAGTCCAAGCCAAAAATTTAAGATGATTTGTCAGAAAGGGCACAAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTATTTTATTTGTGGCAGCTAA
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAATATATTA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATAGCCATTTTCAGTGCAACAAGTAAATCAAAAAGACCATCCTTTATTT
TTCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA
AACTACATTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCTTTTACAAGTTGTAACAACAAAG
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAACTGTGATTTTTTTTCTTCAAGTAAACTTAGT
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAAGTGAAT
AAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTAGAACAAATATGGCATT
TAACCTTATTATTTATTTGCTTTAAGAAATATCTTTGTGGAATTGTTGAATAAACTATAA
AATATTATTTTGATTGCAGCTTTAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

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FIGURE 1B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCTTGAGTGACATTTTAAATA
GAGGAGGTATTCACATATGTTTTCTGTATCACAGCAGCATTCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCTTGACTGTACAAGATTGTTGCAATTTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTCAGG
ANTATATTTTCTACAAGTTCCACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTATCAATTAA

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FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLA AVL LSLCCLLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSS IIFAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTVNLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYEC SAENDVSFPDVRKVKV VVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL
PLNPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

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FIGURE 3

CACTGCCCCGTCCGCTCTTCAGCAGCCGGTCGCGGGCGGTGGAAAAGCGAGTGAAGAGAGCGC
GACGGCGGGCGGGCGGGCGGGCGCAGCTATTGCTGGACGGCCAGTGGGAGAGCGAGGCCTGAG
CCTCTGCGTCTAGGATCAAAATGTTTTCAATCCCAGAATACTATGAAGGCAAGAACGTCCTC
CTCACAGGAGCTACCGGTTTTCTAGGGAAGGTGCTTCTGGAAAAGTTGCTGAGGTCTTGTCC
TAAGGTGAATTCAGTATATGTTTTGGTGAGGCAGAAAGCTGGACAGACACCACAAGAGCGAG
TGGAAGAAGTCCTTAGTGGCAAGCTTTTTGACAGATTGAGAGATGAAAATCCAGATTTTAGA
GAGAAAATTATAGCAATCAACAGCGAACTACCCAACTAACTGGCTCTCAGTGAAGAAGA
TAAAGAGGTGATCATAGATTCTACCAATATTATATTCCACTGTGCAGCTACAGTAAGGTTTA
ATGAAAATTTAAGAGATGCTGTTCAAGTTAAATGTGATTGCAACGCGACAGCTTATTCTCCTT
GCACAACAAATGAAGAATCTGGAAGTGTTTCATGCATGTATCAACAGCATATGCCTACTGTAA
TCGCAAGCATATTGATGAAGTAGTCTATCCACCACCTGTGGATCCCAAGAAGCTGATTGATTCT
TTAGAGTGGATGGATGATGGCCTAGTAAATGATATCACGCCAAAATTGATAGGAGACAGACC
TAATACATACATATACACAAAAGCATTGGCAGAATATGTTGTACAACAAGAAGGAGCAAAAC
TAAATGTGGCAATTGTAAGGCCATCGATTGTTGGTGCCAGTTGGAAAGAACCCTTTCCAGGA
TGGATTGATAACTTTAATGGACCAAGTGGTCTCTTTATTGCGGCAGGGAAAGGAATTCTTCG
AACAAATACGTGCCTCCAACAATGCCCTTGACAGATCTTGTTCCTGTAGATGTAGTTGTCAACA
TGAGTCTTGCGGCAGCCTGGTATTCCGGAGTTAATAGACCAAGAAACATCATGGTGTATAAT
TGTACAACAGGCAGCACTAATCCTTTCCACTGGGGTGAAGTTGAGTACCATGTAATTTCCAC
TTTCAAGAGGAATCCTCTCGAACAGGCCTTCAGACGGCCCAATGTAAATCTAACCTCCAATC
ATCTTTTATATCATTACTGGATTGCTGTAAGCCATAAGGCCCCAGCATTCTGTATGATATC
TACCTCAGGATGACTGGAAGAAGCCCAAGGATGATGAAAACAATAACTCGTCTTCACAAAGC
TATGGTGTTTTCTTGAATATTTCAAGAATAATCTTGGGTTTGGGAATACTGAGAATGTCAATA
TGTTAATGAATCAACTAAACCCTGAAGATAAAAAGACCTTCAATATTGATGTACGGCAGTTA
CATTGGGCAGAATATATAGAGAACTACTGCTTGGGAACCTAAGAAGTACGTATTGAATGAAGA
AATGTCTGGCCTCCCTGCAGCCAGAAAACATCTGAACAAGTTGCGGAATATACGTTATGGTT
TTAATACTATCCTTGTGATCCTCATCTGGCGCATTTTTTATTGCAAGATCACAAATGGCAAGA
AATATCTGGTACTTTGTGGTGTAGTCTGTGTTACAAGTTTTTGTCACTACTTCCGAGCATCCAG
CACTATGAGATAC**TGA**AGACCAAGGATTTCAGCATTAGAACATCTATACATATGGTGATCTAA
ATGTACAAAATGTAAAATGTATAAGTCATCTCACTTTTTTGTCAAGACATTAAACCATCTTAG
ATCGGAGTGTGAAGTAAATTATGGTATATTTTATGTAACATTTTAATGTTTATGCTCATAAA
ACTTAGTGAACACACTGTGTTATGCCAGCTCAAATCTACAGTAGCCACCAAAACCATGACTT
AATATTTTGAGCCCTAGAAGAAAGGGTGTGCTGAGGACAAGAGTGGGGAAATAGGAACACT
GACCAGTATAACTGTGCAATTCTGGAACATATTAATTAATAAATATGCCTTAACATATAGT
GAATTTCTAATTCTAATGTTTCAGTGCAATGGAAGACATTTATTTGGACAGTATACTAGCAAA
GTTGGTAGATATTTGATTCTTCATTTTTTGTTTTTTTTCATTAGTTGAAGTGGGTTTTAGTTT
TGTTTAAAATTATAACCAGCGTATTTTTCACATCATTCTGTAAGTTAAATGATATCAAACATG
AAAGAGATGTTCTCATTTTTCTTTTTCTGATTAAACGTCTGATGCATATCATTTTTCTATAA
GTAATCAGTTGCTTTTAAATCAGAAGGCTATATTATTCTAATGACCCTATTCGATCTAAAT
GGGTTTGAGAATCCATATCAGCAACATACGTGTTTTTTGACAGAAAGTGAAAACAAATCCG
TAAACTGTTAGTATCAAAAAGAATAGGAATACAGTTTTTCTTTTCCACATTATGATCAAATAAA
AATCTTGTGAGATTGTTAAAAA

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FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA94849
><subunit 1 of 1, 515 aa, 1 stop
><MW: 59357, pI: 9.40, NX(S/T): 3
MVSIP EYYEGKNVLLTGATGFLGKVLLEKLLRSCPKVNSVYVLVRQKAGQTPQERVEEVL
SGKLFDRRLRDENPDFREKIIAINSELTQPKLALSEEDKEVIIDSTNIIFHCAATVRFNEN
LRDAVQLNVIATRQLILLAQQMKNLVFMHVSTAYAYCNRKHIDEVVYPPVPDPKKLIDS
LEWMDDGLVNDITPKLIGDRPNTYIYTKALAEYVVQQEGAKLNVAIVRPSIVGASWKEPF
PGWIDNFNGPSGLFIAAGKGILRTIRASNNALADLVPVDVVVNMSLAAAWYSGVNRPRNI
MVYNCTTGSTNPFHWGEVEYHVISTFKRNPLEQAFRRPNVNLTSNHLLYHYWIAVSHKAP
AFLYDIYLRMTGRSPRMMKTITRLHKAMVFLEYFTSNVWVNTENVNMLMNQLNPEDKKT
FNIDVRQLHWA EYIENYCLGTTKYVLNEEMSGLPAARKHLNKLNRNIRYGFNTILVILIWR
IFIARSQMARNIWIYFVVSLCYKFLSYFRASSTMRY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 469-488

N-glycosylation sites:

Amino acids 283-287;304-308;341-345

Tyrosine kinase phosphorylation site:

Amino acids 160-169

N-myristoylation sites:

Amino acids 219-225;252-258;260-266;452-458

Leucine zipper pattern:

Amino acids 439-461

FIGURE 5

[illegible]

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FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96883
><subunit 1 of 1, 514 aa, 1 stop
><MW: 55687, pI: 8.78, NX(S/T): 2
MPAVSGPGPLFCLLLLLLDPHSPETGCPPLRRFEYKLSFKGPRLALPGAGIPFWSHHGDA
ILGLEEVRLTPSMRNRSGAVWSRASVPFSAWEVEVQMRVTGLGRRGAQGMAVWYTRGRGH
VGSVLGGLASWDGIGIFFDSPAEDTQDSPAIRVLASDGHIPSEQPGDGASQGLGSCHWDF
RNRPHSFRARITYWGQRLRMSLNSGLTPSDPGEFCVDVGPLLLVPGGFFGVSAATGTLAG
EDPTGQVPPQPFLEMQQLRLARQLEGLWARLGLGTREDVTPKSDSEAQGEGERLFDLEET
LGRHRRILQALRGLSKQLAQAEQWKKQLGPPGQARPDGGWALDASCQIPSTPGRGGHLS
MSLNKDSAKVGALLHGQWTLQALQEMRDAAVRMAAEQVSYLPVGIHHFLELDHILGL
LQEELRGPAAAAKAPRPPGQPPRASSCLQPGIFLFYLLIQTVGFFGYVHFRQELNKSLO
ECLSTGSLPLGPAPHTPRALGILRRQPLPASPMPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 215-232;450-465

N-glycosylation sites:

Amino acids 75-79;476-480

Glycosaminoglycan attachment site:

Amino acids 5-9

N-myristoylation sites:Amino acids 78-84;122-128;126-132;168-174;172-178;
205-211;226-232;230-236;236-242;356-362**Amidation site:**

Amino acids 102-106

FIGURE 7

[illegible]

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FIGURE 8

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96894
><subunit 1 of 1, 361 aa, 1 stop
><MW: 40747, pI: 9.20, NX(S/T): 1
MAWQGWPAAWQWVAGCWLLLVLVLLVSPRGCRARRGLRGLLMAHSQRLLFRIGYSLYT
RTWLGYLEFYRQQLRRARNRYPKGHSKTQPRLFNGVKVLPPIPVLSDNYSYLIIDTQAQLAV
AVDPSDPRAVQASIEKEGVTLVAILCTHKHWDHSGGNRDLSSRRHRDCRVYGSPQDGIPYL
THPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPIYKGPSCLFSGDLLFLSGCGRTF
EGNAETMLSSLDTVLGLGDDTLLWPGHEYAEENLGFAGVVEPENLARERKMQWVQRQRL
RKGTCPSTLGEERSYNPFLRTHCLALQEALGPGPGPTGDDDISRAQLLEELRRLKDMHKS
K
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

N-glycosylation site:

Amino acids 106-110

Glycosaminoglycan attachment site:

Amino acids 234-238

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 301-305

Tyrosine kinase phosphorylation site:

Amino acids 162-171

N-myristoylation sites:

Amino acids 41-47;235-241;242-248;303-309

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 6-17

cAMP phosphodiesterases class-II proteins:

Amino acids 144-161

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FIGURE 9

GCTGACAATCCCCTTGACGTTCTATCCCGGAAGCTCCACCTGGGGCCCAATGTTGGGCGTGA
TGTTCCCTCGCCTGTCTCTGCCTGGAAAAGTGGTCTTCCCAAGCTCCACTGGCAGCCACTTCT
CCATGTTGGGCATCGGAGACATCGTTATGCCTGGTCTCCTACTATGCTTTGTCTTCGCTAT
GACAACTACAAAAAGCAAGCCAGTGGGGACTCCTGTGGGGCCCCTGGACCTGCCAACATCTC
CGGGCGCATGCAGAAGGTCTCCTACTCTCACTGCACCCTCATCGGATACTTTGTAGGCCTGC
TCACTGCTACTGTGGCGTCTCGCATTACCGGGCCGCCAGCCCGCCCTTCTCTATTTGGTG
CCATTTACTTTATTGCCACTCCTCACGATGGCCTATTTAAAGGGCGACCTCCGGCGGATGTG
GTCTGAGCCTTTTCCACTCCAAGTCCAGCAGCTCCCGATTCTGGAAGT**ATG**ATGGATCACGT
GGAAAGTGACCAGATGGCCGTCATAGTCCTTTTCTCTCAACTCATGGTTTGTTCCTCTTAG
AGCTGGCCTGGTACTCAGAAATGTACCTGTGTTTAAGGAACTGCCGTGTGACTGGATTTGGC
ATTGAAAGGGAGCTCGTTTGCAGGAGAGAGGTGCTGGAGCCCTGTTTGGTTCCTTCTCTTCC
TGCGGATGTAGAGGTGGGGCCCCCTCCAAGAGGGACAGGCCTCTCCCCAGCGCGCCTTCCTC
CCACGTTTTTATGGATCTGCACCAGACTGTTACCTTCTGGGGGAGATGGAGATTGACTGTT
TAAAAAGTGAACAGCGAGGAGTCTTCTAGAACTTTTGAACACTAAAGGATGAAAAAT
TAGC

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FIGURE 10

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA100272
><subunit 1 of 1, 108 aa, 1 stop
><MW: 12055, pI: 4.69, NX(S/T): 0
MMDHVESDQMAVIVLFSQLMVCFLLELAWYSEMYLCLRNCRVTGFGIERELVCRREVLEP
CLVPSPLPADVEVGPLPRGTGLSPARLPPTFLWICTRLLPSGGDGDLTV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-myristoylation site:

Amino acids 80-86

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FIGURE 11

TCGCACACTGGTGGCTTCAGAAGAAATTCCTCAACACCTAGCTCGCCAGAGAGTCTATGTATG
GGATTGAACAATCTGTAAACTAAAGGATCCTAATCATGAAAATAAGTATGATAAATTATAAG
TCACTATTGGCACTGTTGTTTATATTAGCCTCCTGGATCATTTTTACAGTTTTCCAGAACTC
CACAAAGGTTTGGTCTGCTCTAAACTTATCCATCTCCCTCCATTACTGGAACAACTCCACAA
AGTCCTTATCCCTAAACACCACTGATATCATTAAAGCCACTAACAGAGACTGAATCAGA
ATAAAGGAAATCATAGAGAACTAGATCAGCAGATCCCACCCAGACCTTTCACCCACGTGAA
CACCACCACAGCGCCACACATAGCACAGCCACCATCCTCAACCCTCGAGATACGTACTGCA
GGGGAGACCAGCTGCACATCCTGCTGGAGGTGAGGGACCACTTGGGACGCAGGAAGCAATAT
GGCGGGGATTTCTGAGGGCCAGGATGTCTTCCCAGCGCTGATGGCAGGTGCTTCAGGAAA
GGTGACTGACTTCAACAACGGCACCTACCTGGTCAGCTTCACTCTGTTCTGGGAGGGCCAGG
TCTCTCTGTCTCTGCTGCTCATCCACCCAGTGAAGGGGTGTCAGCTCTCTGGAGTGCAAGG
AACCAAGGCTATGACAGGGTGATCTTCACTGGCCAGTTTGTCAATGGCACTTCCCAAGTCCA
CTCTGAATGTGGCCTGATCCTAAACACAAATGCTGAATTGTGCCAGTACCTGGACAACAGAG
ACCAAGAAGGCTTCTACTGTGTGAGGCCTCAACACATGCCCTGTGCTGCACTCACTCACATG
TATTCTAAGAACAAGAAAGTTTCTTATCTTAGCAAAACAAGAAAAGAGCCTCTTTGAAAGGTC
AAATGTGGGTGTAGAGATTATGGAAAAATTCAATACAATTAGTGTCTCCAAATGCAACAAAG
AAACAGTTGCAATGAAAGAGAAATGCAAGTTTGGAAATGACATCCACAATCCCCAGTGGGCAT
GTCTGGAGAAACACATGGAATCCTGTCTCCTGTAGTTTGGCTACAGTCAAATGAAGGAATGC
CTGAGAGGAAAACATATACCTAATGGGAGATTCCACGATCCGCCAGTGGATGGAATACTT
CAAAGCCAGTATCAACACACTGAAGTCAGTGGATCTGCATGAATCTGGAAAATTGCAACACC
AGCTTGCTGTGGATTTGGATAGGAACATCAACATCCAGTGGCAAAAATATTGTTATCCCTTG
ATAGGATCAATGACCTATTCAGTCAAAGAGATGGAGTACCTCACCCGGGCCATTGACAGAAC
TGGAGGAGAAAAAATACTGTCAATTGTTATTTCCCTGGGCCAGCATTTTCAGACCCTTTCCCA
TTGATGTTTTTATCCGAAGGGCCCTCAATGTCCACAAAGCCATTCAGCATCTTCTTCTGAGA
AGCCCAGACACTATGGTTATCATCAAAACAGAAAACATCAGGGAGATGTACAATGATGCAGA
AAGATTTAGTGACTTTTCATGGTTACATTCAATATCTCATATAAAGGACATTTTCCAGGATC
TCAGTGTGAGTATCATTGATGCCTGGGATATAACAATTGCATATGGCACAAATAATGTACAC
CCACCTCAACATGTAGTCGGAAATCAGATTAATATATTATTAACTATATTTGTTAAATAACAA

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FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108696
><subunit 1 of 1, 544 aa, 1 stop
><MW: 62263, pI: 9.17, NX(S/T): 7
MKISMINYKSLALLFILASWIIFTVFQNSTKVWSALNLSISLHYWNNSTKSLFPKTPLI
SLKPLTETELRIKEIIEKLDQQIPPRPFTHVNTTTSATHSTATILNPRDTYCRGDQLHIL
LEVRDHLGRRKQYGGDFLRARMSSPALMAGASGKVTDFNNGTYLVSFRLFEGQVSLSL
LIHPSEGVSALWSARNQGYDRVI FTGQFVNGTSQVHSECGLILNTNAELCQYLDNRDQEG
FYCVRPQHMPCAALTHMYSKNKKVSYLSKQEKSLFERSNVGVEIMEKFNTISVSKCNKET
VAMKEKCKFGMTSTIPSGHVWRNTWNPVSCSLATVKMKECLRGKLIYLMGDSTIRQWMEY
FKASINTLKSVDLHESGKLQHQLAVDLDRNINIQQWKYCYPLIGSMTYSVKEMEYLTRAI
DRTGGEKNTVIVISLGQHFRRPFIDVFIRRALNVHKAIQHLLLRSPDTMVIKTNIREM
YNDARFSDFHGYIQYLIKDIFQDLSVSIIDAWDITIAYGTNNVHPPQHVVGNQINILL
NYIC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 29-33;38-42;47-51;48-52;92-96;160-164;210-214

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 262-266

Tyrosine kinase phosphorylation site:

Amino acids 236-243;486-494

N-myristoylation sites:

Amino acids 206-212;220-226;310-316;424-430;533-539

Amidation site:

Amino acids 127-131

Cell attachment sequence:

Amino acids 113-116

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FIGURE 13

GCAAAGAGAAGACTGAAAGACAAACCTGGGTGCAGCCAGAGAGGTCCAGATAGATGAGCTTG
TGGCATCCATTCCCCAAGTTCAGCCTAGGGACTCCACGTACCCAGCTGGGTCTCATTGTTC
CAGAACTGCATTAGTTAAGATTACCCAGACTTGGATTTCAAAGGAATACTTTCATTGTTCCG
TCTGTAACACGAAGTAATTGGGGCCAGCTGGATGTCAGGATGCGTGTGGTTACCATTGTAAT
CTTGCTCTGCTTTTGCAAAGCGGCTGAGCTGCGCAAAGCAAGCCCAGGCAGTGTGAGAAGCC
GAGTGAATCATGGCCGGGCGGGTGGAGGCCGGAGAGGCTCCAACCCGGTCAAACGCTACGCA
CCAGGCCCTCCCGTGTGACGTGTACACATATCTCCATGAGAAATACTTAGATTGTCAAGAAAG
AAAATTAGTTTATGTGCTGCCTGGTTGGCCTCAGGATTTGCTGCACATGCTGCTAGCAAGAA
ACAAGATCCGCACATTGAAGAACAACATGTTTTCCAAGTTTAAAAAGCTGAAAAGCCTGGAT
CTGCAGCAGAATGAGATCTCTAAAATTGAGAGTGAGGCGTTCTTTGGTTTAAACAAACTCAC
CACCTCTTACTGCAGCACAAACCAGATCAAAGTCTTGACGGAGGAAGTGTTCATTTACACAC
CTCTCTTGAGCTACCTGCGTCTTTATGACAACCCCTGGCACTGTACTTGTGAGATAGAAACG
CTTATTTCAATGTTGCAGATTCCCAGGAACCGGAATTTGGGGAACTACGCCAAGTGTGAAAG
TCCACAAGAACAATAAAAAAATAAAAAACTGCGGCAGATAAAATCTGAACAGTTGTGTAATGAAG
AAAAGGAACAATTGGACCCGAAACCCCAAGTGTGAGGGAGACCCCAAGTCATCAAGCCTGAG
GTGGACTCAACTTTTGGCCACAATTATGTGTTTCCCATACAAACACTGGACTGCAAAGGAA
AGAGTTGAAAAAAGTGCCAAACAACATCCCTCCAGATATTGTTAACTTGACTTGTGATACA
ATAAAATCAACCAACTTCGACCCAAGGAATTTGAAGATGTTGATGAGCTGAAGAAATTAAAC
CTCAGCAGCAATGGCATTGAATTCATCGATCCTGCCGCTTTTTTAGGGCTCACACATTTAGA
AGAATTAGATTTATCAAACAACAGTCTGCAAACTTTGACTATGGCGTATTAGAAGACTTGT
ATTTTTTGAACTCTTGTGGCTCAGAGATAACCCTTGGAGATGTGACTACAACATTCCTAC
CTCTACTACTGGTTAAAGCACCCTACAATGTCCATTTTAATGGCCTGGAATGCAAAACGCCCT
GAAGAATACAAAGGATGGTCTGTGGGAAATATATTAGAAGTTACTATGAAGAATGCCCCAA
AGACAAGTTACCAGCATATCCTGAGTCATTTGACCAAGACACAGAAGATGATGAATGGGAAA
AAAAACATAGAGATCACACCGCAAAGAAGCAAAGCGTAATAATTACTATAGTAGGATTAAGGT
AGAAATTGTTCTGATTGTAATTAGTTTTGTATTTTCTATACTGGTGTAGAAAACATATGTT
TACATTTGATTAACTGTGTTGCCTATTTATGCAGGGTAATCCAGCTAAAGGAAGCTTTCTTT
AATTATAAGTATTATTGTGACTATTATAGTAATCAAGAGAATGCTATCATCCTGCTTGCCTG
TCCATTTGTGGAACAGCATCTGGTGATATGCAATTCACACTGGTAACCTGCAGCAGTTGGG
TCCTAATGATGGCATTAGACTTTCATAATGTCCTGTATAAATGTTTTTACTGCTTTTAGAAA
ATAAAGAAAAAAACTTGGTTCATGTTTAAAA

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FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA117935
><subunit 1 of 1, 440 aa, 1 stop
><MW: 51670, pI: 8.70, NX(S/T): 2
MRVVTIVILLCFCKAAELRKASPGSVRSRVNHGRAGGGRRGSNPVKRYAPGLPCDVYTYL
HEKYLDQCQERKLVYVLPGWPDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQQNEISKI
ESEAFFGLNKLTTLLQHNQIKVLTEEVFIYTPLLSYLRLYDNPDWHCTCEIETLISMLQI
PRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVIKPEVDSTF
CHNYVFPIQTLDCRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFEDVHELKKLNLSS
NGIEFIDPAAFLGLTHLEELDLSNNSLQNFYGVLEDLYFLKLLWLRDNPWRCDYNIHYL
YYWLKHHYNVHFNGLECKTPEEYKGWSVGKYIRSYEECPKDKLPAYPESFDQDTEDEW
EKKHRDHTAKKQSVIITIVG

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 297-301;324-328

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 19-23;39-43;430-434

N-myristoylation sites:

Amino acids 24-30;37-43

Amidation site:

Amino acids 37-41

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FIGURE 15

GCGGCAGCAGCGCGGGCCCCAGCAGCCTCGGCAGCCACAGCCGCTGCAGCCGGGGCAGCCTC
CGCTGCTGTGCGCTCCTCTGATGCGCTTGCCCTCTCCCGGCCCCGGGACTCCGGGAGA**ATGT**
GGGTCCTAGGCATCGCGGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTGCGCTGCAA
ATCCAGTGCTACCAAGTGTGAAGAATCCAGCTGAACAACGACTGCTCCTCCCCCGAGTTCAT
TGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGAAGTGATGGAGCAAAGTGCCG
GGATCATGTACCGCAAGTCCTGTGCATCATCAGCGGCCTGTCTCATCGCCTCTGCCGGGTAC
CAGTCCTTCTGCTCCCCAGGGAACTGAAGTCAAGTTTGCATCAGCTGCTGCAACACCCCTCT
TTGTAAACGGGCCAAGGCCAAGAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGCCAGGGCTCC
GCACCACCATCCTGTTCTCAAATTAGCCCTCTTCTCGGCACACTGCT**TGA**AGCTGAAGGAGA
TGCCACCCCTCCTGCATTGTTCTTCCAGCCCTCGCCCCCAACCCCCACCTCCCTGAGTGA
GTTTCTTCTGGGTGTCCTTTTATTCTGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTGTTCC
TGTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAATAAATTCAGCCTGACTGAATTTTC
AGTATGTACTTGAAGGAAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAACCGGAGT
CAAGGCCAGGCTGGCAGAGTCAGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTA
AGCCTCCAGTGTCCATTCCATCCCTGATGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGA
CGTTTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAACCT
CATGCTCCTGAAAACCATCTCTGCAGCAGAATTGGCTGGTTTCGCGCCTGAGTTGGGCTCT
AGTGACTCGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCCTCGCTCTGAAAAGTGCT
TAAGAAAATCTTCTCAGTTCTCCTTGAGAGGACTGGCGCCGGGACGCGAAGAGCAACGGGC
GCTGCACAAAGCGGGCGCTGTGGTGGTGGAGTGCGCATGTACGCGCAGGCGCTTCTCGTGG
TTGGCGTGCTGCAGCGACAGGCGGCAGCACAGCACCTGCACGAACACCCGCCGAACTGCTG
CGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGA
AGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCC
GCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAG
CCCTGGGCAGACACGAGCAGGAGGGAGAGACAGAGA

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FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119474
><subunit 1 of 2, 141 aa, 1 stop
><MW: 15240, pI: 8.47, NX(S/T): 1
MWVLGIAATFCGLFLLPGFALQIQCYQCEEFQLNNDCCSSPEFIVNCTVNVQDMCQKEVME
QSAGIMYRKSCASSAACLIASAGYQSFCS PGKLN SVCISCCNTPLCNGPRPKKRGSSASA
LRPGLRTTILFLKLALFSAHC

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 45-49

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 113-117

N-myristoylation sites:

Amino acids 5-11;115-121;124-130

Ly-6 / u-PAR domain proteins:

Amino acids 94-107

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FIGURE 17

CGCAAAGCCGCCCTCGGGGCGCTC**ATG**GCGGGACGCCTCCTGGGAAAGGCTTTAGCCGCGGT
GTCTCTCTCTCTGGCCTTGCCCTCTGTGACTATCAGGTCTCGCGCTGCCGCGGCATCCAGG
CGTTCAGAAACTCGTTTTTCATCTTCTTGTTTCATCTTAATACCAACGTCATGTCTGGTTCT
AATGGTTCCAAAGAAAATTCTCACAATAAGGCTCGGACGTCTCCTTACCCAGGTTCAAAAGT
TGAACGAAGCCAGGTTCCCTAATGAGAAAGTGGGCTGGCTTGTTGAGTGGCAAGACTATAAGC
CTGTGGAATACACTGCAGTCTCTGTCTTGCTGGACCCAGGTGGGCAGATCCTCAGATCAGT
GAAAGTAATTTTTCTCCCAAGTTTAACGAAAAGGATGGGCATGTTGAGAGAAAGAGCAAGAA
TGGCCTGTATGAGATTGAAAATGGAAGACCGAGAAATCCTGCAGGACGGACTGGACTGGTGG
GCCGGGGGCTTTTGGGGCGATGGGGCCCAATCACGCTGCAGATCCCATTATAACCAGATGG
AAAAGGGATAGCAGTGGAATAAAATCATGCATCCTGTTTCTGGGAAGCATATCTTACAATT
TGTGTGAATAAAAAGGAAAGACTGTGGAGAATGGGCAATCCCAGGGGGGATGGTGGATCCAGGA
GAGAAGATTAGTGCCACACTGAAAAGAGAATTTGGTGAGGAAGCTCTCAACTCCTTACAGAA
AACCAGTGCTGAGAAGAGAGAAATAGAGGAAAAGTTGCACAACTCTTCAGCCAAGACCACC
TAGTGATATATAAGGGATATGTTGATGATCCTCGAAACACTGATAATGCATGGATGGAGACA
GAAGCTGTGAACTACCATGACGAAACAGGTGAGATAATGGATAATCTTATGCTAGAAGCTGG
AGATGATGCTGGAAAAGTGAAATGGGTGGACATCAATGATAAACTGAAGCTTTATGCCAGTC
ACTCTCAATTCATCAAACCTTGTGGCTGAGAAACGAGATGCACACTGGAGCGAGGACTCTGAA
GCTGACTGCCATGCGTTG**TAG**CTGATGGTCTCCGTGTAAGCCAAAGGCCACAGAGGAGCAT
ATACTGAAAAGAAGGCAGTATCACAGAATTTATACTATAAAAAGGGCAGGGTAGGCCACTTG
GCCTATTTACTTTCAAAACAATTTGCATTTAGAGTGTTTCGCATCAGAATAACATGAGTAAG
ATGAACTGGAACACAAAATTTTCAGCTCTTTGGTCAAAAGGAATATAAGTAATCATATTTTG
TATGTATTGATTTAAGCATGGCTTAAATTAAATTTAAACAATAATGCTCTTTGAAGAATC
ATAATCAGAATAAAGATAAATTCTTGATCAGCTATA

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FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119498
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39125, pI: 8.53, NX(S/T): 2
MAGRLLGKALAAVSLALASVTIRSSRCRGIQAFRNSFSSSWFHLNTNVMSGSNNGSKEN
SHNKARTSPYPGSKVERSQVPNEKVGWLVWQDYKPVEYTAVSVLAGPRWADPQISESNF
SPKFNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGPNHAADPIITRWKR
DSSGNKIMHPVSGKHILQFVAIKRKDCGEWAI PGGMVDPGEKISATLKREFGEEALNSLQ
KTSAEKREIEEKLHKLFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLML
EAGDDAGKVKWVDINDKCLKLYASHSQFIKLVAEKRDHAWSEDSEADCHAL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation site:

Amino acids 55-59

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 179-183

N-myristoylation sites:

Amino acids 53-59;56-62

mutT domain signature:

Amino acids 215-235

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FIGURE 19

CGAGGGCTCCTGCTGGTACTGTGTTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAG
GCCATGCAGCCATGTTCCGGGAGCCCTAATTGCACAGAAGCCC**ATG**GGGAGCTCCAGACTGG
CAGCCCTGCTCCTGCCTCTCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGC
TTTCGCCACCTGCCCCACTGGAACACCCGCTGTCTCTGGCCTCCACACGGATGACAGTTT
CACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTGGTGGGCCCTCTTCTCCACAAAGCCTT
GGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGCTGTCAGGTGGCTCA
GGTCTTCAACGGGGCTCTTCCACCTCCTGGTGCAGAAATCCAAAAAGTCTTCCACATTCAA
GTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTCACC
TGTCTGAGAAGAGCCATCACATTTCCATCCCCCTCCCCAGACATCTCCCACAAGGGACTTCGC
TCTAAAAGGACCCAACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACA
AAGGCATGGAGGACCCGAGTTCTCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTTCGGGTGA
CCATATCTTCAGGCCCTGAGGTACGCGTGCCTTTTGTACCAGTGGGCACTGGAGTGTGAA
GAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTGGGGGCCACACTGTAGAGCTGCC
TTATGAATTCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAAGAGGACACTGTGA
GGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAAGTCA
GTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCC
ACTGAAGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATAACCCTTTGCAAAGACCTCC
CGAATGCCACGGCTCGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCC
CAGCTCTGCTTCAAGTTCTCTTTTGGAAACAGCAGCCATGTTGAATGCCCCCACCAGACTGG
GTCTCTCACATCCTGGAATGTAAGCATGGATACCCAAGCCCAGCAGCTGATTCTTCACTTCT
CCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTCCCAGGCTTGGGGCAGGACACT
TTGGTGCCCCCGTGTACACTGTCAGCCAGGCCCGGGCTCAAGCCCAGTGTCACTAGACCT
CATCATTCCCTTCTGAGGCCAGGGTGCTGTGTCTGGTGTGGCGGTGAGATGTCCAGTTTG
CCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCA
CTGCTGGCCCTCCTCACCTTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTC
AGGCCCGGGCCCAGCGCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGGC
GCCTGGTGGGAGCGCTGGCTGAACTGCTACGGGCAGCGCTGGGCGGCGGGCGCGACGTGATC
GTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGTGGGCCCGCTGCCGTGGCTCTGGGCGGC
GCGGACGCGCGTAGCGCGGAGCAGGGCACTGTGCTGCTGCTGTGGAGCGGCGCCGACCTTC
GCCCCGTGAGCGGCCCCGACCCCCGCGCGCGCCCCCTGCTCGCCCTGCTCCACGCTGCCCGG
CGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGG
ACGCGCGGCCTTTCGCAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCAGCGCAGGCAG
AGCCGCTAGAGCTGTGCAGCCGGCTTGAACGAGAGGCCGCCCCGACTTGACAGACCTAGGT**TG**
AGCAGAGCTCCACCGCAGTCCCGGGTGTCT

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FIGURE 20

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119502
><subunit 1 of 1, 667 aa, 1 stop
><MW: 74810, pI: 9.55, NX(S/T): 3
MGSSRLAALLLP LLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSF TGSSAYIPCRTW
WALFSTKPWCVRVWHCSRCLCQHLLSGGSLQRGLFHLLVQKSKKSSTFKFYRRHKMPAP
AQRKLLPRRHLSEKSHHISIPSPDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFS
FDLLPEARAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLP
CLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQHTQMVMALTLRCPLKLE
AALCQRHDWHTLCKDLPNATARES DGWYVLEKVDLHPQLCFKFSFGNSSHVECPHQTGSL
TSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDL
IIPFLRPGCCVLVWRS DVQFAWKHLCPDVSYRHLGLLILALLLTL LGVVLALTCRRP
QSGPGPARPVLLLHAADSEAQRRLVGALAE LLRAALGGGRDVIVDLWEGRHVARVGPLPW
LWAARTRVAREQGTVLLLWSGADLRPVSGPD PRAAPLLALLHAAPRPLLLLAYFSRLCAK
GDIPPPLRALPRYRLRLRDLPRLLRALDARPF AEATSWGRLGARQRRQSRLELC SRLEREA
ARLADLG
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 455-472

N-glycosylation sites:

Amino acids 318-322;347-351;364-368

Glycosaminoglycan attachment site:

Amino acids 482-486

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 104-108;645-649

Tyrosine kinase phosphorylation site:

Amino acids 322-329

N-myristoylation sites:

Amino acids 90-96;358-364;470-476

Eukaryotic cobalamin-binding proteins:

Amino acids 453-462

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FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119516
><subunit 1 of 1, 172 aa, 1 stop
><MW: 18470, pI: 5.45, NX(S/T): 0
MSSSSGGAPGASASSAPPAQEEGMTWWYRWLCRLSGVLGAVSCAISGLFNCITIHPLNIAA
GVWMIMNAFILLCEAPFCCQFIEFANTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLT
TLLGNAIAFATGVLYGLSALGKKGDAISYARIQQQRQADEEKLAETLEGEL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

Transmembrane domains:

Amino acids 64-77;109-128

Tyrosine kinase phosphorylation site:

Amino acids 142-150

N-myristoylation sites:

Amino acids 5-11;6-12;9-15;35-41;38-44;46-52;124-130;132-138

Amidation site:

Amino acids 140-144

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FIGURE 23

GTGAAACACCCATGGTTTTATGCTCTATTTCTCTTTTCCTCATCTTCTTCCACATCCTCTTT
CTGAATGTATCAAACACTACTTCCTTGAAGTGGGGCACCAGGAGGGCCACTCCAGTCTCCAATG
CAGGGACTCAGGGGCAGGGATCTCTGAGAAAGTGGCCATCTCGTTATTAAAGCTCTGTCCTC
TGCTTCCCTCTCACCTCAGAAGCAGCCCGTTTTATTCAACAGAGCTCCAGGTTGCCAGCTAGG
GGTTTTCGGGACCATAGACCAAGCAACCCGAGAGACTGAGTACTGACCTGCAGTTGTTCCAG
AAACTCTGCTGGGAATTAGGTTGTGACCTAGAAGTGAACTGACACATAACAGTGAGAAGGCAG
GGTAAGAATGCAGTCTAGAGCGCAACCTTTCTCCACTAGACTTGTAAGTAATTTAAGTGAAT
CCTGTCCCCCTGGGGTTCTATCCTGGCTGGCTCTGCTGGTGAACCTGACTGGCCAGCATAGG
GCACTTGATGAGACCCTGGAATGCTGAGGCCAGTTGGGCAGCAAGCTTTCACCTCATCCTTC
TGCCCATCTATCCAGCCATTCAAACATTCATTGCGCTGAAGACATTTATCAAGCTCCTGCAA
TGGGTGAGGCATCTGCTAGGCACTGGGGACACAGAGCTCACAGTCTCCTGGAGGGGGTGAGA
GATGACTGACAGGTGGTCTGTGGTGCAGTGTGACCTGGGAATGCACACAGTACTGTGGAAAC
ACGGGAGAGGCATCTAGCACAACTGAGAGGGCCAGGGGAGGCTTCCTGGCAGGTTTCCCTT
TAACCATCTTAAGGGAAAGAGGCACTAGGTAGGAAAATAAAGGGACAGTGGTGTCCCAGACA
GAGGGCACTCTACATGGAA

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FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119530
><subunit 1 of 1, 113 aa, 1 stop
><MW: 12799, pI: 7.53, NX(S/T): 1
MVLCSISLFLIFFHILFLNVSNYFLEVGHQEGHSSLQCRDSGAGISEKVAISLLKLCPLL
PSHLRSSPFIQQSSRLPARGFRDHRPSNPERLSTDQLFQKLCWELGCDLEVN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 19-23

Glycosaminoglycan attachment site:

Amino acids 41-45

N-myristoylation site:

Amino acids 42-48

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FIGURE 25

CGGGGTCCGCGCGGTCCCACTTCCCGGCTCCCTTCGCCTCCAGGATGCGCTGAGCCCTACAA
CACCCCCAGCGGGCCCGGGCTCCCCACGAGGTGTGAATGACAGAGGTGGTGCCATCCAGCG
CGCTCAGCGAGGTGAGCCTGCGCCTCCTCTGCCACGATGACATAGACACTGTGAAGCACCTG
TGTGGCGACTGGTTCCCATCGAGTACCCAGACTCATGGTATCGTGATATCACATCCAACAA
GAAGTTCTTTTCCCTTGCTGCAACCTACAGAGGTGCCATTGTGGGAATGATAGTAGCTGAAA
TTAAGAACAGGACCAAAATACATAAAGAGGATGGAGATATTCTAGCAACCAACTTCTCTGTT
GACACACAAGTCGCGTACATCCTAAGTCTGGGCGTCGTGAAAGAGTTCAGGAAGCACGGCAT
AGGTTCCCTCTTACTTGAAAGTTTAAAGGATCACATATCAACCACCGCCCAGGACCACTGCA
AAGCCATTTACCTGCATGTCTCACCACCAACAACACAGCAATAAACTTCTATGAAAACAGA
GACTTCAAGCAGCACCCTATCTCCCCTATTACTACTCCATTTCGAGGGGTCCCTCAAAGATGG
CTTCACCTATGTCTCTACATCAACGGCGGGCACCCTCCCTGGACGATTTTGGACTACATCC
AGCACCTGGGCTCTGCACTAGCCAGCCTGAGCCCCTGCTCCATTCCGCACAGAGTCTACCGC
CAGGCCCACAGCCTGCTCTGCAGCTTCCTGCCATGGTCGGGCATCTCTTCCAAGAGTGGCAT
CGAGTACAGCCGGACCATGTGATGTGCGCTGGGCAGCCGCCACCAGGCCCCACCCTTCAGCC
GCCCCGAGAGCCCGCCTTCCTGTCCATCTGACCCCTTCTGTTTTCTGCAAGGAGCTGCCAGC
CATCTAACTGGGCTCGTCGGCCTGCCCCAGCTGCAGGCCCCGGTGCTACACGGGCTCGGGAAC
AGAACATCGTGGGCATGCGCAGAGCATGCCATCCGTGGCAGGCTCTTCAGCTCCCCTCCCT
GCTTCTGGAACCTCTGCCTGCTGCCCTGGCCCTGCCCCCTGCGCATGCACCATCCCCAGG
GCTGACCCAGTGTGGCTGCATTCACTGGGAGGGGCTGCCCTCACTGGGCTCTCCCACTCCG
CTGCCTGTTCTTGACGCTCCTTCCTGGAAAGCTGGAGGGGACTTCTCCTGCAAGGGAGGAA
CGCAAGTATTATGGACACACTTGACCGTAAAGGCACAGGAGCCTCGGAACAAGGGGGCGCAA
TAAAGGGAATGGCCCGTCCCCTTCCAGAACCAGCCCAAAGAAGCCTGGGGGGTGAGGAGTGG
CCCCCACTCCTCCATGAGGGGCTGATGAGGGGTGGGCAGCCTGGGGGAGGCTTCTCCTCGCAA
GCACAGAGCTCTGAGGCTCAGCCCCCTGGCACAGGCGGTACGCATCAGGACGGTTCCTACT
CCTCAGCACCTTCCGTGCAGTTACCAGTGCCCTGGGAGGTCACTGCCCCGTGGACCTTGG
CATGCTCCATTGAGCTGACCTGCTGAGGACAGGCATCGCCGAGACTCCTTGGGTCCTCCCCG
CCCTCCCTCATGCTGCCACAAGCTGCTGCTCCAAGGCCTGGCCACATGCAGACAGGAGGAAG
CTGAGCTCGACATTAGGCCTCAAGGCTGCCATCTGTCTTGTAGGGCCTGGCCTTGTGGGCAG
GGGGCAGTCTGTGCCTTGTGGGCCCTCAGCCTCTGAGGGCAGAGATGCTGTCAGTGCCGCA
GGTGTCATCACATACTTCTAGCATCCTCTCCACCCTGCATTCCAAATGCTGCTTGCTGCCTGC
CCTGCCCTCCGATGCAGGGGTGGGGTGGGGGGCGGAGTCCCGCCCAGCATAGCTGCAGTGTG
ACAAAGCCATGGCAGAGGGTCTAGCGGCGCCACCCTGCCCCAGCCTGAGGAGGAGGGAGAG
GGAGGAACAACCCTGGGCAGACGGGGTCTCAGGGACCTGTGTCCTTCCGCCTCCAGAGCTGC
CCAGCCACGGGCTCTCAGGGTGTGGGGCAGCCCCAGGTCCCCCTCTGAACTCAGCTGGGGC
CAGGGGCCCTCAGAATGAAGGCAGGCACCAGGCAGGAGCAGCATCCCCCTCCTTGACGGTGC
TGGCAGGAGGGCCGCGCCATGCTGACTGCTTGAACCTCTGCTGACCTGACAGTGTGGCGGG
AGGGCCGCACCATGCTGACTGCCTGAATCTCTGCTGAGGCTGCCTGCCTGCCGGGGCCAGCT
CAGCGCCCTCTCCACTGCGAATCAGTGGCGATCATGTGATTTCTATTTCTGCCCCACAGGGT
AAGGGACGAGTCTTCTGGAAGGCTCTGCCATGGACATTTGTCTCGGGCTCAGAGGCCCCAC
CCTGCCCCACACCTGCCCCAATCACTGCAGTGTCCAGCCCAGTGTTGAACAGATTGTAGCG
TTCTGTCTCATTACGAGCAAATAAATAGACTTTCATTGGGAAAAAAAAAAAAA

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FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA121772
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27465, pI: 7.72, NX(S/T): 3
MTEVVPSSALSEVSLRLLCHDDIDTVKHLCDWFPIEYPDSWYRDITSNKKFFSLAATYR
GAIVGMIVAEIKNRTKIHKEDGDILATNFSVDTQVAYILSLGVVKEFRKHGIGSLLES
KDHISTTAQDHCKAIYLVLTNNNTAINFYENRDFKQHHYLPYYYSIRGVKDGFTYVLY
INGGHPPWTILDYIQHLGSALASLSPCSIPHRVYRQAHSLLCSFLPWSGISSKSGIEYSR
TM
```

N-glycosylation sites:

Amino acids 73-77;88-92;143-147

N-myristoylation sites:

Amino acids 61-67;65-71;198-204;235-241

Matrixins cysteine switch motif:

Amino acids 18-31

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FIGURE 27

GTTGGGCAGCAGCCACCCGCTCACCTCCATCCCCAGGACTTAGAGGGACGCAGGGCGTTGGG
AACAGAGGACACTCCAGGCGCTGACCCTGGGAGGCCAGGACCAGGGCCAAAGTCCCGTGGGC
AAGAGGAGTCCTCAGAGGTCCTTCATTCAGCGGTTCCGGGAGGTCTGGGAAGCCCACGGCCT
GGCTGGGGCAGGGTCAACGCCGCCAGGCCGCCATGGTCTGTGCTGGCTGCTGCTTCTGGTG
ATGGCTCTGCCCCAGGCACGACGGGCGTCAAGGACTGCGTCTTCTGTGAGCTCACCGACTC
CATGCAGTGTCTGGTACCTACATGCACTGTGGCGATGACGAGGACTGCTTCACAGGCCACG
GGGTCGCCCCGGGCACTGGTCCGGTCATCAACAAAGGCTGCCTGCGAGCCACCAGCTGCGGC
CTTGAGGAACCCGTCAGCTACAGGGGCGTCACCTACAGCCTCACCACCAACTGCTGCACCGG
CCGCCTGTGTAACAGAGCCCCGAGCAGCCAGACAGTGGGGGCCACCACCAGCCTGGCACTGG
GGCTGGGTATGCTGCTTCCTCCACGTTTGCTGTGACCAACAGGGAGGACAGGGCCTGGGACT
GTTCTCCCAGATCCGCCACTCCCCATGTCCCATGTCTTCCCCACTAAATGGCCAGAGAG
GCCCTGGACAACCTCTTGCGGCCCTGGCTTCATCCCTTCTAAGGCTGTCCACCAGGAGCCCG
GTGCTAGGGGAAGCATCCCCAGGCCTGACTGAGCGGCAGGGGAGCACGGCCCGTGGGTTTGA
TTGTATTACTCTGTTCCACTGGTTCTAAGACGCAGAGCTTCTCACATCTCAATCAGGATGCT
TCTCTCCATTGGTAGCACTTTAGAGTCCATGAAATATGGTAAAAAATATATATATATCATAA
TAAATGACAGCTGATGTTTCATGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125148
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13004, pI: 5.70, NX(S/T): 0
MVLCLLLLLVMALPPGTTGVKDCVFCELTDSMQCPGYMHCGDDEDCFTGHGVAPGTGPV
INKGCLRATSCGLEEPVSYRGVTYSLTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLP
PRL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-13

N-myristoylation sites:

Amino acids 19-25;52-58;64-70;81-87;106-112

Ly-6 / u-PAR domain proteins:

Amino acids 84-97

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FIGURE 29

GGCATT TTTGAAAGCCCAGTGT TGCCAGGGGGCATCTCCTTTGTGTTTATGAGAGACCTGCA
TTCTCCCTGGCTCAGTTCTCTCAGGCTCTCCAGAGCTCAGGACCTCTGAGAAGAATGAGGCC
CTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTCTGCATGTCTC
TGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATCAGAGCCCTGCAC
CTGTTTCCTGCACCCCTGCCACTGGTTCTATGGCCACAAGGAGTTTTACCCAGTAAAGGA
GTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTTCCCTTGTGGGTGGAC
CCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAGATTCTCCTGAAAAGACAA
GATCCCAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGGGTGGTCGAGGACTTGTGAC
CCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTGAAACCTGGCTTCAACATCAGCA
TTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTTCGGATGATGCTGAACAAATGGGAG
GAACACATTGCCCAAACCTCACGTCTGGAGCTCTTCAACATGTCTCCTGATGACCCTGGA
CAGCATCATGAAGTGTGCCTTCAGCCACCAGGGCAGCATCCAGTTGGACAGTACCCTGGACT
CATACTGAAAGCAGTGTTCACCTTAGCAAAATCTCCAACCAGCGCATGAACAATTTTCTA
CATCACAACGACCTGGTTTTCAAATTCAGCTCTCAAGGCCAAATCTTTTCTAAATTTAACCA
AGAACTTCATCAGTTCACAGAGAAAGTAATCCAGGACCGGAAGGAGTCTCTTAAGGATAAGC
TAAACAAGATACTACTCAGAAAAGGCGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAA
AGCGAAAACACCAAAGATTTCTCTGAAGCAGATCTCCAGGCTGAAGTGAACGTTTCATGTT
TGCAGGACATGACACCACATCCAGTGCTATCTCCTGGATCCTTTACTGCTTGGCAAAGTACC
CTGAGCATCAGCAGAGATGCCGAGATGAAATCAGGGAACCTAGGGGATGGGTCTTCTATT
ACCTGGGAACACCTGAGCCAGATGCCTTACACCACGATGTGCATCAAGGAATGCCTCCGCCT
CTACGCACCGGTAGTAAACATATCCCGGTTACTCGACAAACCCATCACCTTTCCAGATGGAC
GCTCCTTACCTGCAGGAATAACTGTGTTTATCAATATTTGGGCTCTTCACCACAACCCCTAT
TTCTGGGAAGACCTCAGGTCTTTAACCCCTTGAGATTCTCCAGGGAAAATTCTGAAAAAAT
ACATCCCTATGCCTTCATACCATTTCTCAGCTGGATTAAGGAACTGCATTGGGCAGCATTTTG
CCATAATTGAGTGTAAGTGGCAGTGGCATTAACCTCTGCTCCGCTTCAAGCTGGCTCCAGAC
CACTCAAGGCCTCCCCAGCCTGTTTCGTCAAGTTGTCCTCAAGTCCAAGAATGGAATCCATGT
GTTTGCAAAAAAAGTTTGCTAAATTTTAAGTCCTTTCGTATAAGAATTAATGAGACAATTTTCT
ACCAAAGGAAGAACAAAAGGATAAATATAATACAAAATATATGTATATGGTTGTTTGACAAA
TTATATAACTTAGGATACTTCTGACTGGTTTTTGACATCCATTAACAGTAATTTTAATTTCTT
TGCTGTATCTGGTGAAACCCACAAAAACCTGAAAAAATCAAGCTGACTTCCACTGCGAA
GGGAAATTATTGGTTTGTGTAAGTAGTGGTAGAGTGGCTTTCAAGCATAGTTTGATCAAAAC
TCCACTCAGTATCTGCATTACTTTTATCTCTGCAAATATCTGCATGATAGCTTTATTCTCAG
TTATCTTTCCCCATAATAAAAAATATCTGCCAAA

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FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125150
><subunit 1 of 1, 505 aa, 1 stop
><MW: 59086, pI: 9.50, NX(S/T): 3
MEPSWLQELMAHPFLLLLILLCMSLLLQVIRLYQRRRWMIRALHLFPAPPAHWFYGHKEF
YPVKEFEVYHKLMEKYPCAVPLWVGPFMTMFFSVHDPDYAKILLKRQDPKSAVSHKILESW
VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMMSESVRMMLNKWEEHIAQNSRLELF
QHVSMLTLD SIMKCAF SHQSGIQLDSTLDSYLKAVFNLSKISNQRMNFLHHNDLVFKFS
SQGQIFSKFNQELHQFTEKVIQDRKESLKDCLKQD TTQKRRWDFLDILLSAKSENTKDFS
EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQQRCDREIRELLGDGSSITWEHLS
QMPYTTMCIKECLRLYAPVVNISRLLDKPI TFPDGRSLPAGITVFINIWALHHPYFWED
PQVFNPLRFSRESENKIHPIYAFIPFSAGLRNCIGQHFAIIECKVAVALTLRFLAPDHS
RPPQPVRRQVVLKSKNGIHVFAKKVC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 451-470

N-glycosylation sites:

Amino acids 145-149;217-221;381-385

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 264-268

N-myristoylation sites:

Amino acids 243-249;351-357;448-454;454-460

Cytochrome P450 cysteine heme-iron ligand signature:

Amino acids 445-455

Cytochrome P450 cysteine heme-iron ligand proteins:

Amino acids 442-473

FAD-dependent glycerol-3-phosphate dehydrogenase proteins:

Amino acids 124-141

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FIGURE 31

TCCGCTGTCGCCCAGTCCCGGCCGCTGGCGGGAAGTACCTGGAGCAAGCAGGACCTTCCCT
CCCACCTCTCCCGCCTGGCCTCCGCGGGAGTCCCCTACGATCCCGCTCAGCAGTGGGGCACT
CGCTGAGGACAGCGAGTCCTGGGAGTGAGCCCAAGGCCACCCCTGGCCAGCCCAGGAGAGAT
AGCCAGGGCAGGCCCAGCAGCCCCGAGGCCAGGCTCTGGCCACGGCGGTCTCCGAC**ATGG**AGA
GACATTGTCTGCTTTTTATCCTGTAACTGTCTTCGGTGGTTGTGCCACGACATTCCCCAG
GGTTCAGGTGCCCAGGTGGCCGAGGGTCAGTCCAGTGGTAGAGCCTTGCTCTCCTAGGCTCAT
CCTGCTGGCGGTCTCTGCTTCTGCTGTGTGGTGTACAGCTGGTTGTGTCCGGTTCTGCT
GCCTCCGGAAGCAGGCACAGGCCAGCCACATCTGCCACCAGCACGGCAGCCCTGCGACGTG
GCAGTCATCCCTATGGACAGTGACAGCCCTGTACACAGCACTGTGACCTCCTACAGCTCCGT
GCAGTACCCACTGGGCATGCGGTTGCCCTGCCCTTTGGGGAGCTGGACCTGGACTCCACGG
CTCCTCCTGCCTACAGCCTGTACACCCCGAGCCTCCACCCTCCTACGATGAAGCTGTCAAG
ATGGCCAAGCCCAGAGAGGAAGGACCAGCACTCTCCAGAAACCCAGCCCTCTCCTTGGGGC
CTCGGGCCTAGAGACCACTCCAGTGCCCCAGGAGTCGGGCCCCAATACTCAACTACCACCTT
GTAGCCCTGGTGCCCCCT**TGA**AGGAGGTAGGAGAACGGACCAGAGCTTGGAGAACTAATGCTT
GGAGCCAAGGGCCCCAGCCCACCCACCGTCCCACACATTGCTGTGGCCCCAACCTCGGTGC
CATGTTACACCGGCCCTGGCGTCACCCACTAGGCAGGCTGCTGCTTTCAGCCTCAGCCCCT
GGCCCAGCCCCAGCAGGCCCTCAGCCTGGAAGAGGCCCTTGGGCCTAAGCCTCGGGTGGGA
GCTCAGGGCCACCTGTGACGTCTGCATCTTCTTGGAGAGAGAATAAAGTTGTATTTAAGTGGT

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FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125151
><subunit 1 of 1, 194 aa, 1 stop
><MW: 20882, pI: 6.44, NX(S/T): 0
MERHCLLFILLTCLRWLCHDIPQGSGARWPRVSPVVEPCSPRLILLAVLLLLLCGVTAGC
VRFCCLRKQAQAQPHLPPARQPCDVAVIPMDSDSPVHSTVTSYSSVQYPLGMRLPLPFGE
LDLDSTAPPAYSlytPEPPPSYDEAVKMAKPREEGPALSQKPSPLL GASGLETT PVPQES
GPNTQLPPCSPGAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 39-58

N-myristoylation site:

Amino acids 55-61

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 50-61

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FIGURE 33

CCTTGCTTGGTGCTTGGCACACACAAATCCAGTGGGCTACACAGGTTTTCCAGAAGCCCCAC
GAGGTGGTAATGGTGCTGCTGATTGAGACCCTGGGGGCCCTCATGCCCTCGCTGCCCTCCTG
CCTCAGCAACGGCGTGGAGAGGGCAGGGCCCGAGCAGGAGCTCACCAGGCTGCTGGAGTTCT
ACGACGCCACCGCCCACTTCGCCAAGGGCTTGGAGATGGCACTGCTCCCCACCTACATGAA
CACAATCTGGTAAAAGTCACGGAGCTGGTGGATGCTGTGTATGATCCATACAAACCCTACCAG
CTGAAGTATGGCGACATGGAAGAGAGCAACCTCCTCATCCAGATGAGTGCTGTGCCTCTGGA
GCATGGGGAAGTGATTGACTGTGTGCAGGAGCTGAGCCACTCCGTGAACAAGCTGTTTGGTC
TGGCGTCTGCAGCCGTTGACAGATGCGTCAGATTACCAATGGCCTGGGGACCTGCGGCCTG
TTGTGAGCCCTGAAATCCCTCTTTGCCAAGTATGTGTCTGATTTACCAGCACTCTCCAGTC
CATACGAAAGAAGTGCAAACCTGGACCACATTCCCTCCCAACTCCCTCTTCCAGGAAGATTGGA
CGGCTTTTCAGAACTCCATTAGGATAATAGCCACCTGTGGAGAGCTTTTGCGGCATTTGTGGG
GACTTCGAGCAGCAGCTAGCCAACAGGATTTTGTCCACAGCTGGGAAGTATCTATCTGATTC
CTGCAGCCCCCGGAGCCTGGCTGGTTTTTCAGGAGAGCATCTTGACAGACAAGAAGAACTCTG
CCAAGAACCCTATGGCAAGAATATAATTACCTCCAGAAAGATAAACCTGCTGAATATGCCAGT
TTAATGGAAATACTTTATACCCTTAAGGAAAAAGGGTCAAGCAACCACAACCTGCTGGCTGC
ACCTCGAGCAGCGCTGACTCGGCTTAACCAGCAGGCCCACCAGCTGGCTTTTCGATTCCGTGT
TCCTGCGCATCAAACAACAGCTGTTGCTTATTTTGAAGATGGACAGCTGGAATACGGCTGGC
ATCGGAGAAACCCTCACAGATGAACTGCCCCGCTTTAGTCTCACCCCTCTCGAGTACATCAG
CAACATCGGGCAGTACATCATGTCCCTCCCCCTGAATCTTGAGCCATTTGTGACTCAGGAGG
ACTCTGCCTTAGAGTTGGCATTGCACGCTGGAAAGCTGCCATTTCCCTCCTGAGCAGGGGGAT
GAATTGCCCCGAGCTGGACAACATGGCTGACAACCTGGCTGGGCTCGATCGCCAGAGCCACAAT
GCAGACCTACTGTGATGCGATCCTACAGATCCCTGAGCTGAGCCCACACTCTGCCAAGCAGC
TGGCCACTGACATCGACTATCTGATCAACGTGATGGATGCCCTGGGCCTGCAGCCGTCCCGC
ACCCTCCAGCACATCGTGACGCTACTGAAGACCAGGCCTGAGGACTATAGACAGGTCAGCAA
AGGCCTGCCCCGTGCGCTGGCCACCACCGTGGCCACCATGCGGAGTGTGAATTACTGAACCCC
ACCACACACCGGACCACCAAGAGAGCCAGGGCTGCTGTTTCGTGACTCACCAGCACAGATTT
GCTCAGAACTCTGCCCCAAGATTGGGCAGAAGTTACTTTAAAAAGACTTGGTTTCAGCTGGTC
ACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGCCAGATGGATCATGAGGCC
AGGAGTTCGAGACCAGCCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAAT
TAACAGCAGAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGACTTGGTTTCATTTGTATAA
TCAAAAAGAGTTGTAAATTAAAGATGTATTATTTATCAGAGAAGACTTTTTAGATAATTTTT
TTAAAGGATCAGATCTTGAAAATGGAATAAATAACTACTGTGAAATGCAAAA

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FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125181
><subunit 1 of 1, 491 aa, 1 stop
><MW: 54759, pI: 5.61, NX(S/T): 0
MVLLIQTLGALMPSLPSCLSNGVERAGPEQELTRLLEFYDATAHFAKGLEALLPHLHEH
NLVKVTELVDVYDPYKPYQLKYGDMEESNLLIQMSAVPLEHGEVIDCVQELSHSVNKL
GLASAAVDRCVRFTNGLGTCGLLSALKSLFAKYVSDFTSTLQSIRKKCKLDHIPPNSLFQ
EDWTAFQNSIRIIATCGELLRHCGDFEQQLANRILSTAGKYLSDCSPRSLAGFQESILT
DKKNSAKNPWQEYNYLQKDNPAEYASLMEILYTLKEKGSSNHNLLAAPRAALTRLNQQA
QLAFDSVFLRIKQQLLLISKMDSWNTAGIGETLTDELPAFSLTPLEYISNIGQYIMSLPL
NLEPFVTQEDSALELALHAGKLPFPPEQGDELPELDNMADNWLGSARATMQTYCDAILQ
IPELSPHSAKQLATDIDYLINVMDALGLQPSRTLQHVITLLKTRPEDYRQVSKGLPRRLA
TTVATMRSVNY
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 242-246

N-myristoylation sites:Amino acids 22-28;48-54;121-127;136-142;141-147;328-334;
447-453**Leucine zipper pattern:**

Amino acids 295-317

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FIGURE 35

GCAAGTGCCACCATGCTAGTGTGATTTGGACTTCAGTAAAAGTTAGTTTGCTTCCTTCCCGT
TGTCCCATCTCACTCCTGGGCCACCC**ATG**GGGCTGCTGGTAGCTGGTGTGTGGCTGCTGCTG
GACTGTGTGGCAGTCCATCCATCTGTTCAGCAGCCACTGCGGGCCTACTTGCTGGGTGCCCAG
CACCGCACTCACCCTGCAGGCGTGGCCAGGAGCGTGAGATCCCCAGAGCCCATGGCCAGTG
AGAGGCGGCCAGGGATAGGTACCCAGGGAATGCCACAGGAGTTTGCTGGGCTCACGGAGCTC
TTTCACTGGTCAGAGAGGAGTGTGTGTAGGAGAGGACTTCTACTTGGTGTGAAGGACAGAT
GGGGTTTGGCTGGGAGAGAGGAGGAATGTGGGCGGGCCTTATAGGCAGGCGAGAAGGTGAGA
GCCAAGGCCCTCTGTGGGCAGGGCGAGGTGGCGTGTTGAGGAGACTCGTCCAGCTGGGCAGA
GGCTCATGT**TGA**GGGATGAGGCAGAGCTGGGGGAGGAGGGAGCCCAGAAATGGCAGGTCCTT
GAATGCAGGTTTGGGAAGCAGGGACGCCCTGTGAGGGTACAGAGTCTGGGCTGTTACCTTCTG
TGGCTTTTGCTAGAAGGTGAGATGTCAGGGAGGAAGACAGGACTCCAGGATGTCTCCTGTCTCT
CTCTGGAAAAAGGAGGTGGGCCCCCTTCTCAGCAGTCAGCTGCTGTTTTTGAGGTCTTCTCC
ATGGATAATCCACGGTGTTGGAAGTGGTTAAGGTAATGGATCCTCATGGGCTTACCATAAAA
ATATCTGGAGGCTGGACCATTTTCCTTAAACGTTATAAAAGCTGGAATTGAATGCCATCGG
TGTCACCCCTGGGAAGTGTGCTTTCTCTTGAGCTCTTTTGGCCCCGAGATAGCAGTCACTCC
ATAGTTTCGTGAAGACCAGCCTGGTGTTCCTGGTTTTCTGCCATTAGGGAGCAGCTAGAGG
TCTTCCAGTAGCTCCTGTGTAAAGTGATGAAAGAAAAGGGCTGGGTGCTGACTGCTCCTGGA
GAAAAGCAACACACTCCCAAAGTCTTAATTGCCTGCTTCCAGGGAGCTGTGGTGGTTTCCCT
TGGGCAGGGCACACGCCCCAGTGGTTGACTTAATAAGGATACATTTTAATCAGAGGACAAAA
ATGTGCCCTGACTTGATTTCCGCATGGGCTTCCAGCATGGTCAAAGG

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FIGURE 36

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125192
><subunit 1 of 1, 139 aa, 1 stop
><MW: 14841, pI: 9.20, NX(S/T): 0
MGLLVAGVWLLLDCAVHPSVSSHCGPTCWVPSTALT TAGVARSVRSPEPMASERRPGIG
TQGMPQEFAGLTELFHWSERSVCRRGLLLGVEGQMFGWERGGMWAGLIGRREGESQGPI
WAGRGGVLRRLVQLGRGSC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 2-8;40-46;86-92;102-108;103-109

Amidation site:

Amino acids 109-113

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FIGURE 37

GGCCAGGA**AT**GGGGTCCCCGGGCATGGTGCTGGGCCTCCTGGTGCAGATCTGGGCCCTGCAA
GAAGCCTCAAGCCTGAGCGTGACGAGGGGGCCCAACTTGCTGCAGGTGAGGCAGGGCAGTCA
GGCGACCCTGGTCTGCCAGGTGGACCAGGGCCACAGCCTGGGAACGGCTCCGTGTTAAGTGGACA
AAGGATGGGGCCATCCTGTGTCAACCGTACATCACCAACGGCAGCCTCAGCCTGGGGGTCTG
CGGGCCCCAGGGACGGCTCTCCTGGCAGGCACCCAGCCATCTCACCCCTGCAGCTGGACCCTG
TGAGCCTCAACCACAGCGGGGCGTACGTGTGCTGGGCGGCCGTAGAGATTCTGAGTTGGAG
GAGGCTGAGGGCAACATAACAAGGCTCTTTGTGGACCCAGATGACCCACACAGAACAGAAA
CCGGATCGCAAGCTTCCCAGGATTCTCTTCGTGCTGCTGGGGGTGGGAAGCATGGGTGTGG
CTGCGATCGTGTGGGGTGCCTGGTTCTGGGGCCGCCGAGCTGCCAGCAAAGGGACTCAGGA
AATGCATTCTACAGCAACGTCCTATAACCGCCCCGGGGGGCCCCAAAGAAGAGTGAGGACTG
CTCTGGAGAGGGGAAGGACCAGAGGGGCCAGAGCATTTATTCAACCTCCTTCCCGCAACCGG
CCCCCGCCAGCCGCACCTGGCGTCAAGACCCTGCCCCAGCCCGAGACCCTGCCCCAGCCCC
AGGCCCCGGCCACCCCGTCTCTATGGTCAGGGTCTCTCCTAGACCAAGCCCCACCCAGCAGCC
GAGGCCAAAAGGGTTCCCCAAAGTGGGAGAGGAG**TGA**GAGATCCCAGGAGACCTCAACAGGA
CCCCACCCATAGGTACACACAAAAAAGGGGGGATCGAGGCCAGACACGGTGGCTCACGCCTG
TAATCCCAGCAGTTTGGGAAGCCGAGGCGGGTGAACACTTGAGGTCAGGGGTTTGAGACCA
GCCTGGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAG
CCTGGGCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAACAAGCAGGAGGATTGGGAGCC
TGTCAGCCCCATCCTGAGACCCCGTCCTCATTTCTGTAATGATGGATCTCGCTCCCACTTTC
CCCCAAGAACCTAATAAAGGCTTGTGAAGAAAAAAAAAAAAAAAAA

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FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125196
><subunit 1 of 1, 278 aa, 1 stop
><MW: 30319, pI: 9.21, NX(S/T): 3
MGSPGMVLGLLVQIWALQEASSLSVQQGPNLLQVRQGSQATLVCQVDQATAWERLRVKWT
KDGAILCQPYITNGSLSLGVCGPQGRLSWQAPSHLTQLDPVSLNHSGAYVCWAAVEIPE
LEEAEGNITRLFVDPDDPTQNRNRISFPGFLFVLLGVGSMGVAAIVWGAWFWGRRSCQQ
RDSGNAFYSLNLYRPRGAPKKSEDCSGEGKDQRGQSIYSTSFPQPAPRQPHLASRPCSP
RPCPSRPGHPVSMVRVSPRPSPTQQPRPKGFPAKVGE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

Transmembrane domain:

Amino acids 149-166

N-glycosylation sites:

Amino acids 73-77;105-109;127-131

Glycosaminoglycan attachment site:

Amino acids 206-210

N-myristoylation sites:

Amino acids 5-11;37-43;63-69;108-114

Amidation site:

Amino acids 173-179

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FIGURE 39

[illegible]

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FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125200
><subunit 1 of 1, 290 aa, 1 stop
><MW: 32335, pI: 5.82, NX(S/T): 1
MPLLTLYLLLFWLSGYSIATQITGPTTVNGLERGLTVQCVRSGWETYLKWWCRGAIWR
DCKILVKTSQSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT
VQVTIDPAPVTQEETSSSPTLTGHHLDNRHKLLKLSVLLPLIFTILLLLLVAASLLAWRM
MKYQQKAAGMSPEQVLQPLEGDLQCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA
SLPKEDISYASLTLAGAEDQEPTYCNMGHLSSHLPGRGPPEEPTYSTISR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domain:

Amino acids 155-174

N-glycosylation site:

Amino acids 88-92

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 218-222

Tyrosine kinase phosphorylation site:

Amino acids 276-285

N-myristoylation sites:

Amino acids 30-36;109-115;114-120

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FIGURE 41

AAGAACACTGTTGCTCTTGGTGGACGGGCCCAGAGGAATTCAGAGTTAAACCTTGAGTGCCT
GCGTCCGTGAGAATTCAGC**ATGGA**ATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTG
CAAGATTGCCACTTGATGCCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCT
GCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGA
AAAACCTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCC
GTGTGCAGGCGGTCTGACCAGTGA CTACCCAGCCCTCGTGGGCTCAAATATAACATTTGCG
GTGAACCTGATATTCCTTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAA
GAACTGCAGAAATGAGGCTGGTTTATCTGCTGATCCGTATGTTTACAACCTGGACAGCATGGT
CAGAGGACAGTGACGGGGAAAATGGCACC GGCCAAAGCCATCATAACGTCTTCCCTGATGGG
AAACCTTTTCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTT
GGTCAGTATTTCCAGAAATTGGGACGATGTTTCACTGAGAGTTTCTGTGAACACAGCCAATGT
GACACTTGGGCTCAACTCATGGAAGTGA CTGTCTACAGAAGACATGGACGGGCATATGTTT
CCATCGCACAAGTGAAAGATGTGTACGTGGTAACAGATCAGATTCCTGTGTTTGTGACTATG
TTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCTCAAAGATCTCCCCATTATGTT
TGATGTCCTGATTCATGATCCTAGCCACTTCTCAATTATTCTACCATTAACTACAAGTGGA
GCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTG
CTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCC
ACCGCCACCACCACCCAGACCTTCAAACCCACCCCTTCTTTAGCAACTACTCTAAAATCTT
ATGATTCAAACACCCACCCAGGACCTACTGGTGACAACCCCTGGAGCTGAGTAGGATTCCTGAT
GAAAACCTGCCAGATTAAACAGATATGGCCACTTTCAGCCACCATCACAATTGTAGAGGGAAT
CTTAGAGGTTAACATCATCCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCT
CCCTAATAGACTTTGTGCTGACCTGCCAAGGGAGCATTCCCACGGAGGTCTGTACCATCATT
TCTGACCCACCTGCGAGATCACCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGAT
GTGTCGTCTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCC
TGGGGGATGACACAAGCCTGGCTCTCACGAGCACCCCTGATTTCTGTTCTTGACAGAGACCCA
GCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTGGCTGCTTGGCCATATTTGT
CACTGTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTC
CTGGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAAGCCGTGTTT
TTCCCGGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCT**TA**
AATTTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTG
GCTATTAACCTTTTTTCTTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGA
ATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTC
AGCCATGTTGTGAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTCATTATTTTTTATGTT
TCACTTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAG
AAGCTACTATTGATTAGAGCCTAACCAGGTTAACTGCAAGAAGAGGCGGGATACTTTTCAGC
TTTCCATGTAAGTGTATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTA
ACTGAATCCCACTTCAATACACACTCATGAACCTCTGATGGAACAATAACAGGCCCAAGCCT
GTGGTATGATGTGCACACTTGCTAGACTCAGAAAAATACTACTCTCATAAATGGGTGGGAG
TATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCAATTA
TTCCATGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGT
GTATATTTCCAAATTTTTGTACAGTCGCTGCACATATTTGAAATCATATATTAAGACTTTCC
AAAGATGAGGTCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTACCTCTGTTTGTA
ACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCCTTCCTGAAAAATAAA
GTGTGGGAAGAGACA

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FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125214
><subunit 1 of 1, 572 aa, 1 stop
><MW: 63953, pI: 6.55, NX(S/T): 12
MECLYYFLGFLLLAARLPLDAAKRFHDVLGNERPSAYMREHNQLNGWSSDENDWNEKLYP
VWKRGD MRWKN SWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIVYEKNC
RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVPDGGKPFPHHPGWRRWNFIYVFHTL
GQYFQKLGRCSVRVSVNTANVTLG PQLMEVTVYRRHGRAYVPIAQVKDVYVVT DQIPVFV
TMFQKNDRNSSDETFLKDLPI MFVDVLIHDP SHFLNYSTINYKWSFGDNTGLFVSTNHTVN
HTYVLNGTFSLNLT VKAAAPGPCPPPPPPRPSKPTPSLATTLKSYDSNTPGPTGDNPLE
LSRIPDENCQINRYGHFQATITIV EGILEVNI IQMTDVLMPVPWPPESSLIDFVVT CQGS I
PTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLT LGDDTSLALTS
TLISVPDRDPASPLRMANSALISVGCLAI FVTVISLLVYKKHKEYNPIENSPGNVVR SKG
LSVFLNRAKAVFFPGNQEKDPLLKNQEFKGVS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 496-516

N-glycosylation sites:Amino acids 93-97;134-138;146-150;200-204;249-253;275-279;
296-300;300-304;306-310;312-316;459-463;467-471**N-myristoylation sites:**

Amino acids 91-97;147-153;290-296;418-424

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 496-507

Cell attachment sequence:

Amino acids 64-67

FIGURE 43

[illegible]

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FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125219
><subunit 1 of 1, 283 aa, 1 stop
><MW: 31175, pI: 7.51, NX(S/T): 0
MADPHQLFDDTSSAQSRGYGAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQ
GKELVDKNIDRFIPITKLKYYFAVDTRYVGRKLGLLFFPYLHQDWEVQYQQDTPVAPRFD
VNAPDLYIPAMAFITYVLVAGLALGTQDRFSPDLLGLQASSALAWLTLEVLAILLSLYLV
TVNTDLTTIDLVAFLGYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLKI
LADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFLVLR
```

Important features of the protein:**Transmembrane domain:**

Amino acids 126-142;164-179;215-233

N-myristoylation sites:

Amino acids 54-60;141-147;156-162;201-207;205-211;209-215

Amidation site:

Amino acids 89-93

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FIGURE 45

GCTGAGCACCAACAGGAACTATTCCAGTGAAGAGCAAGTGCTGCCCGACCCAGGACCCTGTG
CCAGGCTGGCAGCCCTCCAGCTCCCTCCAGAGAGGAAACCTCTGTCTGGCTGAGGGTGGGAC
TAGCTGGGATGTCTCACTCCAGTTGCTCAGGTTCACCCAGGAAGCTCCTCCGTGGAGTGGCC
AGCCTGATTCTAGCCCTGTCTCTCTGGCAGCACATGCCACACCTGCCTGGGCCTTCTGCTC
CCTGATGCTTGATGAGCCCCTGCCTCCTCAATGTTTCTCAAAGACAGACCCCCCTGAGGCCAGC
TTGAATGTGAAGACTGCTGAAGTCAGCTGGCTTCACTTGAGCTGCAGAAAAGGTGGCTGGGA
TGGCCCAGGTGCACCCAGAGGCCCCAGCCCTTTGGCTGCCTTTGGGTTGTGACTTGGGTTGT
CTCTGAGGCCCTGCCAGAGCTGGGCCTGCGGGTGGTGGGCGGTCCGACCTCGGGCAGTCAGT
GCTCCGCAGCCTCAGCACTGCATCCCAGACCCAGTGTCCTCAGAGGGAAGAGCCAGCCTCCC
TGCCTCATGGAACCAGGAGTCCCCAAAAGTCAGGAGCCTGGAGGCTCTGAAAGGAGCAGGGA
TTCCATAGTGCGTGAAGCTGAAATAGGCGCCCTCCTGGGGAGCCCCCAGCAAAACTGTTTTT
CATACCCACTCCCAGAACTGCCCCGCTCCAGCTCCAGCGCCAGCGCCAGCTGGTTGCCAGGC
GTCATTGGAGAGGCCTGGCTGCCCCAGGGGCAGCAGGGAGTGGTGGACCTGTATGGGCTGGC
AGGAGGCCATTGGCCATGCTGACAAGTGTACCTGCCTTCCTAGCCTGGAGCCACCCCTCAG
GTGGCCTGCTTGACCTCCTATCCGGAGGTAGCCTGCCCCACCTGTAGGCAGAGGGGGCTCT
TGCTTGAGGCCTGCACAGGAAGCAAGTATAGCCCCGGTGCCCCAGAGTGGGTCCACTTAGC
CCTGGCGAGATGGCCTGTCCTGAGATCTCTGCTCCAGACCCACCATCTGGGGAGCACAGT
CCTTAGGCTGCCTGGTCCAGGAAGGGGTGCGGCTCTGTGAGGAAACCTGGACTCTCAAGGC
CCACCAGCCTCTCCGTGAGTGTTAGAAATCACAGATACAGTATATACTTAATTACACTACTC
ACTACTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 46

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA128309
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10112, pI: 8.64, NX(S/T): 0
MSHSSCSGSPRKLLRGVASLILALSSLAHATPAWAFCSLMLDEPLPPQCFSKTDPPPEAS
LNVKTAEVSWLHLSCRKGGWDGPGAPRGPSPLAAFGI
```

Important features of the protein:

Signal peptide:

Amino acids 1-31

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FIGURE 47

TTCCGGGGCCCTGGCGTCTCGTCTCCTTACCCTGGGGCTACCCTTGCCCCGGTCCTACTGCCCG
CGGTAAACCCGCCGCGAGCCGCCTCTCCCCTCCCCGCCCCGACTCAACCCTGCCCTCCCCCGT
GCTTTGCAGACGCCGCCCGGGGGCCCAGGCGGCTG**ATG**CGTGTGGGCCTCGCGCTGATCTTG
GTGGGCCACGTGAACCTGCTGCTGGGGGCCGTGCTGCATGGCACCGTCCTGCGGCACGTGGC
CAATCCCCGCGGCGCTGTCACGCCGGAGTACACCGTAGCCAATGTCATCTCTGTGCGGCTCGG
GGCTGCTGAGCGTTTCCGTGGGACTTGTGGCCCTCCTGGCGTCCAGGAACCTTCTTCGCCCT
CCTGCTGACTGGGTCTGCTGGCACTAGCTCTGGTGAACCTGCTCTTGTCGGTTGCCTGCTC
CCTGGGCCTCCTTCTTGCTGTGTCACTCACTGTGGCCAACGGTGGCCGCCGCCCTTATTGCTG
ACTGCCACCCAGGACTGCTGGATCCTCTGGTACCACTGGATGAGGGGCCGGGACATACTGAC
TGCCCCCTTGACCCCAAGAATCTATGATACAGCCTTGGCTCTCTGGATCCCTTCTTTGCT
CATGTCTGCAGGGGAGGCTGCTCTATCTGGTTACTGCTGTGTGGCTGCACTCACTCTACGTG
GAGTTGGGCCCTGCAGGAAGGACGGACTTCAGGGGCAGCTAGAGGAAATGACAGAGCTTGAA
TCTCCTAAATGTAAAAGGCAGGAAAATGAGCAGCTACTGGATCAAAATCAAGAAATCCGGGC
ATCACAGAGAAGTTGGGTT**TAG**GACAGGTGCTGTTCCGAGACTCAGTCCTAAAGGGTTTTTT
TTCCCCTAAGCAAGGGGCCCTGACCTCGGGATGAGATAACAAATTGTAATAAAGTAACTTC
TCTTTTCTTCTAAA

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FIGURE 48

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129535
><subunit 1 of 1, 222 aa, 1 stop
><MW: 23566, pI: 6.70, NX(S/T): 0
MRVGLALILVGHVNLLLGAVLHGTVLRHVANPRGAVTPEYTVANVISVGSGLLSVSVGLV
ALLASRNLLRPPLHWVLLALALVNLLLSVACSLGLLLAVSLTVANGGRRRIADCHPGLLD
PLVPLDEGPGHTDCPFDPTRIYDTALALWIPSLMSAGEAALSGYCCVAALTLRGVGPCR
KDGLQGQLEEMTELESPKCKRQENEQLLDQNQEIRASQRSWV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 44-60;76-96

N-myristoylation sites:

Amino acids 94-100;175-181

Amidation site:

Amino acids 106-110

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 81-92

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FIGURE 49

CGTCAGTCTAGAAGGATAAGAGAAAAGAAAGTTAAGCAACTACAGGAAATGGCCTTTGGGAG
TTCCAATATCAGTCTATCTTTTATTCAACGCAATGACAGCACTGACCGAAGAGGCAGCCG
TGACTGTAACACCTCCAATCACAGCCCAGCAAGCTGACAACATAGAAGGACCCATAGCCT
TGAAGTTCTCACACCTTTGCCTGGAAGATCATAACAGTTACTGCATCAACGGTGCTTGTG
CATTCCACCATGAGCTAGAGAAAAGCCATCTGCAGGTGTTTTACTGGTTATACTGGAGAAA
GGTGTGAGCACTTGACTTTAACTTCATATGCTGTGGATTCTTATGAAAAATACATTGCAA
TTGGGATTGGTGTTGGATTACTATTAAGTGGTTTTCTTGTTATTTTTTACTGCTATATAA
GAAAGAGGTATGAAAAAGACAAAATATTGAAGTCACTTCATATGCAATCGTTTGACAAATA
GTTATTCAGGCCCTATAATGTGTCAGGCACTGACATGTAAAATTTTTTTAATTAAAAAAG
AGCTGTAATCTGGCAAAAAGTTTCTATGTAATATTTTTCATGCCTTTTCTCATAAACCCA
GACGAGTGGTAAAAATTTGCCTTCAGTTGTAATAGGAGAGTTCAAACGTACAGTCTCCCT
TCAACCTATCTCTGTCTGCCCATATCAAATTATAAATGAGGAGGACAGCAGGCCCAAG
AAAGTAGGGACTAAGTATGTCTTGTTCAAATTGTATATTCAGTGACTTACACTATGCCT
AGCACACAACACACACTGAGTAAATATTTGTTGAGTGAAATAAAATCAAGAAACAAGTAA
AAACTGA

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FIGURE 50

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129549
><subunit 1 of 1, 133 aa, 1 stop
><MW: 14792, pI: 5.97, NX(S/T): 0
MALGVPISVYLLFNAMTALTEEA AVTVTPPITAQQADNIEGP IALKFSHLCLEDHNSYCI
NGACAFHHELEKAICRCFTGYTGERCEHLTLTSYAVDSYEKYIAIGIGVGLLLSGFLVIF
YCYIRKRYEKDKI
```

Important features of the protein:**Signal peptide:**

1-20 (weak)

Transmembrane domain:

103-117

N-myristoylation site.

4-10;106-112;110-116

EGF-like domain cysteine pattern signature.

75-87

Integrins beta chain cysteine-rich domain proteins

66-88

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FIGURE 52

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129580
><subunit 1 of 1, 114 aa, 1 stop
><MW: 12886, pI: 7.04, NX(S/T): 0
MQIQNNLFFCCYTVMSAIFKWLLLYSLPALCFLLGTOESESFHSKAEILVTLSQVIISPA
GPHALTWTTHFSPSVIIILVPCWWHAVIVTQHPVANCYVTNHLNIQWLELKAGS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-33

Transmembrane domain:

Amino acids 71-86

N-myristoylation site:

Amino acids 35-41

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FIGURE 53

TTTTGAAATGGTTT**ATG**ACCTCTTCCCCACTTCCCCGCTTGCTTTGCTCATTAGTGTTCCCTA
GGTGGCTGCTGGGTGACGGGCTTTTCATCATCTCTGATGTGGGCCAGTGCGAAAGAGCAGCT
GCAACATCTGTTTCTAATTGGGTCGTGCCTTTATAAATACTTCTTGCCATTTTGTACATTG
CTTCCCTCCCACCTGTCTTCCTTGGAGTACTGCAGAATCTGTAAGCGTCCCTGGAATGCAC
ACGTGGACCTTGTCATTCCCAAACAGACTTTCTGCTGGTCAGCACTTTGTAATGTTCGGCTG
TTACAGGCAT**TAGT**CACTTGCTGCTCAGAGAGAGACTGTGGTCTTTGGAACTGAAGAAAATGTC
TTTTTTGTTGTTGTTAATTCTTGGCATCCAGTTAGATTTAACTTCTCAAGAGTTTACACAGA
CTTTTAGAAAAACATTCTGTCTCTAAGAAAAAAGTGCTCTAGCTTTGTACAGTTTTTGGATT
TTCACACTTGGTGGTTGTTTGCTGAAATGCTGTTTTGCTAGTGATTCCCCCTCTCCCCCTAT
CTGGGGTTGTAAGCAGCTCTGGGGCTCTGTTCACTTCGGATACCTGTTTCTGGGGACTGCTT
TTCAACAGCGTTTTTCCTAAGGGCATATGAGAAATTTAATTTCTGATGGAATGAAGGTGAAA
CTCTAGTCCCAGGTAAACCTGGGTAGGCTGTAGAGACAGAAAGGGGGCTGCAGGTCTAGGTG
GAAGAACGAGAACGAATGCAGCATGGTATTTCCAGGCCTTTTAGATTCTGGCTTCATCCACAA
CCAATGTGAGTTCTTATCTGCAAAGCGGGCCTAAGTGTAATGGAGGGAAGGTGGGCCAGGCA
CCAGGGTCCTGGGTCTCCCGCGCCTCACTCTGTCTCCACCTGGCCCATGCATAAAGAACAC
TAGTCAAGTAGCCATTGTACCTGTTTCCTTATCTGAAAATGAGAAGGTTGGAGAGTATGACT
TCTGTTGAAACAACAAGGCGCTTACAAATTTTGGTGAAGTCGAATGAGGCGAGCGTTAAGAG
AAATATCAAAGTTAGTCATTGGATTTTCAAGGCTTAGGGATGGAAACCAGCTGGTAGTAGACT
GGTTGTAGTTATGTCCAAGGGCAGAGTGGGAAAAATTTGGCCGAAAAGAGTGTGGTGGGTG
ACCAGCAAATGTTAGAGGTATACATCAGGGCACAGAGGAGAAAAGCTAACATGATACTGATG
ACTTCAAGTCTTCACTGTCCAATTCAGAGGATAGGGGAGGGTTTAAGCTGATTAAACAGTGG
GCTTTTTTTCTCCTGCAAGAGGGTGGAGGTCTATAACTGTGCAGATTTTATCAGATGCATGC
TAATACATGTTATTCTGGGGGACTCTCTTATACCTTGAAGTAGACATTGCTGCTATTTGCGT
GAAAAAATAGGAGGACTTATTTGAATTGAGAATGGGGATAGGCTGAGTTCCACCGAGATGT
TGGCTTAGAGATGCCTGGGCCATGCTGTACAGTAGGAAGCCCAGCAGAGGAGATTGGGCTGT
GTGGGTCATGACAAAGGGAGTTGTTAGCTTATGGTTGGCTATTAAAGTCATGGGCAAGGATG
GGCAAGAAAAGTGTGTAAAATGAGCTGACAAAAGATAAATATGTTAATTA

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FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129794
><subunit 1 of 1, 102 aa, 1 stop
><MW: 11382, pI: 8.72, NX(S/T): 0
MTSSPLPRLLCSLVFLGGCWVTGFSSSLMWASAKEQLQHLFLIGSCLYKYFLPICHIASL
PPCLPWSTAESVSVPGMHTWTLSFPNRLSAGQHFVMFGCYRH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

N-myristoylation site:

Amino acids 18-24

Prokaryotic membrane lipoprotein lipid attachment sites:Amino acids 9-20;36-47;
89-100

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FIGURE 55

ACACTGGCCAAACACTCGCATCCCAGGGCGTCTCCGGCTGCTCCCATTTGAGCTGTCTGCTCG
CTGTGCCCCGCTGTGCCTGCTGTGCCCCGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGACGCG
GGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCG
AGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTC
CTGGGTGGTGTTCATCCCCCTTGGGGCTGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCT
GCCCAACGTCACTCTCTTAGAGGAGCTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCC
GGGTCCGCAGAGCCATCCCCAGGGAGGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTT
CGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACATGACCTGGGATGACGAACTGGA
GAAGTCTGCTGCAGCGTGGGCCAGTCAGTGCATCTGGGAGCACGGGCCCCACGAGTCTGCTGG
TGTCCATCGGGCAGAACCTGGGCGCTCACTGGGGCAGGTATCGCTCTCCGGGGTTCCATGTG
CAGTCTTGGTATGACGAGGTGAAGGACTACACCTACCCCTACCCGAGCGAGTGAACCCCTG
GTGTCCAGAGAGGTGCTCGGGGCCTATGTGCACGCACTACACACAGATAGTTTGGGCCACCA
CCAACAAGATCGGTTGTGCTGTGAACACCTGCCGGAAGATGACTGTCTGGGAGAAGTTTGG
GAGAACGCGGTCTACTTTGTCTGCAATTATTCTCCAAAGGGGAAGTGGATTGGAGAAGCCCC
CTACAAGAATGGCCGGCCCTGCTCTGAGTGCCCAACCAGCTATGGAGGCAGCTGCAGGAACA
ACTTGTGTTACCGAGAAGAAACCTACACTCCAAACCTGAAACGGACGAGATGAATGAGGTG
GAAACGGCTCCCATTCCTGAAGAAAACCATGTTTGGCTCCAACCGAGGCTGATGAGACCCAC
CAAGCCCAAGAAAACCTCTGCGGTCAACTACATGACCCAAGTCGTCAGATGTGACACCAAGA
TGAAGGACAGGTGCAAAGGGTCCACGTGTAACAGGTACCAAGTGCAGCAGGCTGCCTGAAC
CACAAGGCGAAGATCTTTGGAAGTCTGTTCTATGAAAGCTCGTCTAGCATATGCCGCGCCGC
CATCCACTACGGGATCCTGGATGACAAGGGAGGCCTGGTGGATATCACCAGGAACGGGAAGG
TCCCCTTCTTCGTGAAGTCTGAGAGACACGGCGTGCAGTCCCTCAGCAAATACAAACCTTCC
AGCTCATTTCATGGTGTCAAAAGTGAAAGTGCAGGATTTGGACTGCTACACGACCGTTGCTCA
GCTGTGCCCCGTTTGAAAAGCCAGCAACTCACTGCCCAAGAATCCATTGTCCGGCACACTGCA
AAGACGAACCTTCCTACTGGGCTCCGGTGTGTTGGAACCAACATCTATGCAGATACCTCAAGC
ATCTGCAAGACAGCTGTGCACGCGGGAGTCATCAGCAACGAGAGTGGGGGTGACGTGGACGT
GATGCCCCGTGGATAAAAAGAAGACCTACGTGGGCTCGCTCAGGAATGGAGTTCAGTCTGAAA
GCCTGGGGACTCCTCGGGATGGAAAGGCCTTCGGGATCTTTGCTGTGAGGCAG**TGA**ATTTCC
AGCACCAGGGGAGAAGGGGCGTCTTCAGGAGGGCTTCGGGGTTTTGCTTTTATTTTATTTT
GTCATTGCGGGGTATATGGAGAGTCA

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FIGURE 56

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131590
><subunit 1 of 1, 497 aa, 1 stop
><MW: 55906, pI: 8.43, NX(S/T): 4
MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNESSHVRRAIPREDKEEIL
MLHNKLRGQVQPQASNMEYMTWDDELEKSAAAWASQCIWEHGPTSLLVSIGQNLGAHWGR
YRSPGFHVQSWYDEVKDYTYYPSECNPWCPERCSPMCTHYTQIVWATTNKIGCAVNTC
RKMTVWGEVWENAVYFVCNYSKGNWIGEAPYKNGRPCSECPPSYGGSCRNNLCYREETY
TPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDRCKG
STCNRYQCPAGCLNHKAKIFGSLFYESSSSICRAAIHYGILDDKGGLVDITRNGKVPFFV
KSERHGVQSLSKYKPSSSFMVSKVKVQDLDCYTTVAQLCPFEKPATHCPRIHCPAHCKDE
PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDVMPVDKKKTYVGSLRNGVQSES
LGTPRDGKAFRIFAVRQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 27-31;41-45;451-455

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 181-185;276-280;464-468

Tyrosine kinase phosphorylation site:

Amino acids 385-393

N-myristoylation sites:Amino acids 111-117;115-121;174-180;204-210;227-233;300-306;
447-453;470-476**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

Amino acids 195-207

SCP-like extracellular protein:

Amino acids 56-208

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FIGURE 57

GCACGAGGCCAAACACAGCAGCCTCAACATGAAGGTGGTTATGGTCCTCCTGCTTGCTGCCC
TCCCCCTTTACTGCTATGCAGGTTCTGGTTGCGTTCTTCTGGAGAGCGTCGTGGAAAAGACC
ATCGATCCATCGGTTTTCTGTGGAGGAATACAAAGCAGATCTTCAGAGGTTTCATCGACACTGA
GCAAACCGAAGCAGCTGTAGAGGAGTTCAAGGAGTGCTTCCTCAGCCAGAGCAATGAGACTC
TGGCCAACTTCCGAGTCATGGTGCATACGATATATGACAGCCTTTACTGTGCTGCGTATTAA
CTGTCACAAGAACTTTGGCTCAGAGGAATCCAGACGATGCTCACAACCCGACTGTGGACTGG
CAGAAATCTCAACTTTTCCTTTTGACTTTCCCCTTTGATCAGTAATATGGAAGACGTTGTTG
AAACCTGAAGTATAGTTAATTTAAATAAACCCACTGCAAGAAAAAAAAAAAA

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FIGURE 58

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA135173
><subunit 1 of 1, 93 aa, 1 stop
><MW: 10456, pI: 4.37, NX(S/T): 1
MKVVMVLLLAALPLYCYAGSGCVLLESVVEKTIDPSVSVEEYKADLQRFIDTEQTEAAVE
EFKECFLSQSNETLANFRVMVHTIYDSLYCAAY
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 12-23

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FIGURE 59A

CAAGTCCGTTGAGGCTGCCAGGCGAGTCAGGTCTCTCTGGACCTCGCCTGACTCGGCTGGGC
TGTGCCTGAAATTGACCCAGCTCCACCATACTCCTTGATT**ATG**AGAAAACAAGGAGTAAGCT
CAAAGCGGCTGCAATCTTCCGGCCGAGCCAGTCTAAGGGGCGGCGGGGGCCTCCCTCGCC
CGGGAGCCGGAGGTAGAGGAGGAGGTGGAAAAGTCGGTCCTAGGCGGCGGGAACTGCCAAG
GGGCGCCTGGAGGTCTCCCCGGGGAGGATCCAAAGTCTGAAAGAGCGAAAAGGCTTGGAGC
TAGAGGTGGTGGCCAAGACCTTTCTTCTCGGCCCTTCCAGTTCGTCCGTAATTCCCTGGCG
CAGCTCCGGGAAAAGGTGCAGGAAGTGCAGGCGCGGCGGTCTCCAGCAGAACCCTCTCGG
CATCGCTGTCTTTGTGGCAATTTTACATTGGTTACATTTAGTAACACTTTTTGAAAATGATC
GTCATTTCTCTCACCTCTCATCTTTGGAACGGGAGATGACTTTTCGCACTGAAATGGGACTT
TATTATTCATACTTCAAGACCATTATTGAAGCACCTTCGTTTTTGGAGGACTGTGGATGAT
TATGAATGACAGGCTTACTGAATATCCTCTTATAATTAATGCAATAAAACGCTTCCATCTTT
ATCCAGAGGTAATCATAGCCTCCTGGTATTGCACATTCATGGGAATAATGAATTTATTGGGA
CTAGAAACTAAGACCTGCTGGAATGTCACCAGAATAGAACCTCTTAATGAAGTTCAAAGCTG
TGAAGGATTGGGAGATCCTGCTTGCTTTTATGTTGGTGTAATCTTTATTTTAAATGGACTAA
TGATGGGATTGTTCTTCATGTATGGAGCATACTGAGTGGGACTCAACTGGGAGGTCTTATT
ACAGTACTGTGCTTCTTTTCAACCATGGAGAGGCCACCCGTGTGATGTGGACACCACCTCT
CCGTGAAAGTTTTTCTATCCTTTTCTTGTACTTCAGATGTGTATTTTAACTTTGATTCTCA
GGACCTCAAGCAATGATAGAAGGCCCTTCATTGCACTCTGTCTTTCCAATGTTGCTTTTATG
CTTCCCTGGCAATTTGCTCAGTTTATACTTTTTACACAGATAGCATCATTATTTCCCATGTA
TGTTGTGGGATACATTGAACCAAGCAAATTTCAGAAGATCATTTATATGAACATGATTTAGTT
ACCCCTTAGTTTTATTTTGTGTTTGGAAATTCAATGTACTTATCTTCTTATTATTCTTCATC
TTTGTTAATGACGTGGGCAATAATTCTAAAGAGAAATGAAATTCAAAACTGGGAGTATCTA
AACTCAACTTTTTGGCTAATTCAAGGTAGTGCCTGGTGGTGTGGAACAATCATTTTGAATTT
CTGACATCTAAAATCTTAGGCGTTTTAGACCACATTCGCCTGAGTGATCTTATAGCAGCCAG
AATCTTAAGGTATACAGATTTTGATACTTTAATATATACCTGTGCTCCCGAATTTGACTTCA
TGGAAAAAGCGACTCCGCTGAGATACACAAAGACATTATTGCTTCCAGTTGTTATGGTGATT
ACATGTTTTATCTTTAAAAAGACTGTTCTGTGATATTTTCATATGTTTTAGCTACAAACATTTA
TCTAAGAAAACAGCTCCTTGAACACAGTGAGCTGGCTTTTCACACATTGCAGTTGTTAGTGT
TTACTGCCCTTGCCATTTTAATTATGAGGCTAAAGATGTTTTTGACACCGCACATGTGTGTT
ATGGCTTCCTTGATATGCTCTCGACAGCTCTTTGGCTGGCTTTTTTCGCAGAGTTCGTTTTGA
GAAGGTTATCTTTGGCATTTTAACAGTGATGTCAATACAAGGTTATGCAAACCTCCGTAATC
AATGGAGCATAATAGGAGAATTTAATAATTTGCCTCAGGAAGAACTTTTACAGTGGATCAAA
TACAGTACCACATCAGATGCTGTCTTGCAGGTGCCATGCCTACAATGGCAAGCATCAAGCT
GTCTACACTTCATCCCATTGTGAATCATCCACATTACGAAGATGCAGACTTGAGGGCTCGGA
CAAAAATAGTTTTATTCTACATATAGTCGAAAATCTGCCAAAGAAGTAAGAGATAAATTGTTG
GAGTTACATGTGAATTATTATGTTTTAGAAGAGGCATGGTGTGTTGTGAGAATAAGCCTGG
TTGCAGTATGCTTGAAATCTGGGATGTGGAAGACCCCTCCAATGCAGCTAACCCCTCCCTTAT
GTAGCGTCCTGCTCGAAGACGCCAGGCCTTACTTCACCACAGTATTTCAGAATAGTGTGTAC
AGAGTATTAAAGGTTAACT**AG**AGAAGGATACTACCCATTTTACTATGGCACAATGCCGTGTGT
CAAAAACAATCACCCCTTTGGCTTATTACATTAATAAAAAATCACAGCTTTAATAACAGACA
CTTAAAAATAAGATAAAAAATGGATTGGAAATTTTTCTGATTACTAAAAGGTAATTACTTTTT
CTGTTTCAATGAATGTCAGCCTTATTAAGCTTGTATATAAGTTATTAAATCAATTCATGTCAT
ACTGCATAAACAAATGTTCAATTTTCAAGATTTTAAAGAGAAATGTATATAAAGAACMATGATT
TTAATAATCAGGGGTATGTAAGTCCTTTTTTCATCCAAGTGAATTGCTTCAGATTTTCT
CTAGTACCAGAGGGTACCTCCTCAAACTCTTTGAACCACTTAAGGCAGAAGAATGCAAGCTC
TGAAATGACATCCTTAAATGCTGATACTGGTCACAGCCTCTTTACCTCTGTGAGGAAATTG
TAACAGTGTGTCTTTTAAGGTGTTTTTATTTTACCAGCCCTTAAGAAAGATCTCTAATACCT
TTTTAATACTTTTTTTTAAATAATTTCAAGTTGAAGTGTTTTTAAAAACACTTTGTTTTGTAAT
GTTTTGAATCTCTTGAGATGTGTTTACCCCACTAGATACATATTTGCCACTGGTTAGTTCTC
CATCTAAGCTCAAGAGGTTATTCATCTCTCTTTAGATTCCAGTGGCTTTTCTTTTAAACATCC
AGGTAAAACAGAACTGCTATGGTATACAACCAAGTTTTTGGGGTTAAACATAATCAGAAAAG

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FIGURE 59B

AAAATCCAGTTAAATTTATGAAGTGAGATTTTCAGATCCTAGATCTTGAATAAAGGAAAGGT
CTTTTCATCTTGATGGCCCCAAAGCTTGTTGGTCATGGTCTTTATTTCTGGCCACTATCTTC
TTAAATAATATATTTTTAAGCCCTCATTTATTTTTGGTTTTGGGTGAGGAAAGTCATGTTTT
CTAAGTCCTCTCCCCTAATAAAACCTACCCAACAATAGTGCTTTGAAAAGTGGTAGTTATCT
TGAAGATACTCTTGCCAAATGCAAAGATAAACATTCTTTTTGTCTGCTTTATAAATATGAAA
TATGCCAGATCTATAGTATTTTAATGTGCATCTACTTTAAATGAGTCATCTTGGGGTTTTTA
TAATTCCTTATGTTCTTGCCCTCTACACTTGAAATAACAAAATGCCTTAATTTTATGGAT
TAGTTCTCTTATAGTAGACAGGCAGCTATATGCAGCAAACCAATAAAGTTATTTTTCAACT
TTCATAGTTGTAAATATCTTATACCAGAATACAAAACAGCTAAGAAAACATGCCACATTTTAT
TTTAGCATTTTCAAATAATTTGTTTTTGGTGTAAGCACAGGATAAAAAAGGAGAGCGTCAAA
GAAAAGAGACATAACACCTAACATTCATAAAAATTAACAAAGTATATTTTGGATGATGTTTT
TACAGGAAATATTTTAAATAAGTTGGTAGAACTTTTAAAATGGTACTGTATTAGCTAATAAA
ATATTCAGTACAAATATATGTTTGGATTTATGCATTAAAAAACTAATAAAATTATTTCCAAC
TTTA

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FIGURE 60

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA138039
><subunit 1 of 1, 758 aa, 1 stop
><MW: 87354, pI: 9.36, NX(S/T): 1
MRKQGVSSKRLQSSGRSQSKGRRGASLAREPEVEEEVEKSVLGGGKLPRGAWRSSPGRIQ
SLKERKGGLELEVVAKTFLLGPFQFVRNSLAQLREKVQELQARRFSSRTTLGIAVFVAILH
WLHLVTLFENDRHFSHLSSLEREMTFRTMGLYYSYFKTIIIEAPSFLEGLWMIMNDRLTE
YPLIINAIKRFLHYPEVIIASWYCTFMGIMNLFGLTKTCWNVTRIEPLNEVQSCEGLGD
PACFYVGVIFILNGLMMGLFFMYGAYLSGTQLGGLITVLCFFFNHGEATRVMWTPPLRES
FSYPFLVLQMCILTILRTSSNDRPFIALCLSNVAFMLPWQFAQFILFTQIASLFPMYV
VGYIEPSKFQKIIYMNMISSVTLSFILMFGNSMYLSSYYSSSLMTWAIILKRNEIQKLG
SKLNFWLIQGSAAWCGTIIILKFLTSKILGVSDHIRLSDLIAARILRYTDFDTLIYTCAPE
FDFMEKATPLRYTKITLLPVVMVITCFIFKKTVRDISYVLATNIYLRKQLEHSELAFHT
LQLLVFTALAILIMRLKMFLTPHMCVMASLICSRQLFGWLFRRVRFEKVI FGILTVMSIQ
GYANLRNQWSIIGEFNNLPQEELLQWIKYSTTS DAVFAGAMPTMASIKLSTLHPIVNHPH
YEDADLRARTKIVYSTYSRKSACEVRDKLLELHVNYVLEEAWCVVRTKPGCSMLEIWDV
EDPSNAANPPLCSVLLEDARPYFTTVFQNSVYRVLKV
```

Important features of the protein:**Transmembrane domain:**

Amino acids 109-124;197-213;241-260;266-283;302-315;336-356;
376-391;430-450;495-509;541-560;584-599;634-647

N-glycosylation site:

Amino acids 222-226

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 102-106

Tyrosine kinase phosphorylation site:

Amino acids 511-519

N-myristoylation sites:

Amino acids 24-30;50-56;151-157;254-260;264-270;269-275;
273-279;639-645

Amidation site:

Amino acids 20-24

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FIGURE 61

GGCGCGGCCACATCCTTTAAATATGGTCTTTCTTGGGCGCGCGCGACAATGTGAGGAGTGGG
GTGGAGCGTGTGTGGTGTGTGGCTGCGGCCTGGGCAAGAGCCGCCGCGGACCATGAGCTGAG
TAAGTTCTGGAGGGATCCTGCCTCTTGGAGCCTTCGCAGCCAGGCAGCTGTGAAGTGTGAGC
TAGAGTGAAGCAGAAATCTAGGAAGATGAGCTCCAAGATGGTCATAAGTGAACCAGGACTGA
ATTGGGATATTTCCCCCAAAATGGCCTTAAGACATTTTTCTCTCGAGAAAATTATAAAGAT
CATTCCATGGCTCCAAGTTTAAAAGAAGTACGTGTTTTATCCAACAGACGTATAGGAGAAAA
TTTGAATGCCTCAGCAAGTTCTGTAGAAAATGAGCCGGCAGTTAGTTCAGCAACTCAAGCAA
AGGAAAAAGTTAAAACCACAATTGGAATGGTCTTCTTCCAAAACCAAGAGTTCCTTATCCT
CGTTTCTCTCGTTTCTCACAGAGAGAGCAGAGGAGTTATGTGGACTTGTGGTTAAATACGC
AAAGATTCTGCAAATTCCAAAGCTGTTGGAATAAATAAAAAATGACTACTTGCAGTACTTGG
ATATGAAAAACATGTGAACGAAGAAGTTACTGAGTTCCTAAAGTTTTTGCAGAATTCTGCA
AAGAAATGTGCGCAGGATTATAATATGCTTTCTGATGATGCCCGTCTCTTCACAGAGAAAAT
TTTAAGAGCTTGCATTGAACAAGTGAAGAAAGTATTGAGAAATCTATACTCTCCACGAGGTCA
CCAGCTTAATGGGATTCTTCCCATTTCAGAGTAGAGATGGGATTAAAGTTAGAAAAAACTCTT
CTCGCATTGGGCAGTGTAAAATATGTGAAAACAGTATTTCCCTCAATGCCTATAAAGTTGCAG
CTGTCAAAGGACGATATAGCTACCATTGAAACGTGAGAACAAACAGCTGAAGCTATGCATTA
TGATATTAGTAAAGATCCAAATGCAGAGAAGCTTGTTTCCAGATATCACCTCAGATAGCTC
TAACTAGTCAGTCATTATTTACCTTATTAATAATCATGGACCAACGTACAAGGAACAGTGG
GAAATTCAGTGTGTATTCAAGTAATACCTGTTGCAGGTTCAAACCAGTTAAAGTAATATA
TATTAATTCACCACTTCCCCAAAAGAAAATGACTATGAGAGAGAGAAAATCAAATCTTTTCATG
AAGTTCCATTAATAATTTATGATGTCCAAAACACATCTGTTCCAGTCTCTGCAGTCTTTATG
GACAAACCTGAAGAGTTTATATCTGAAATGGACATGTCTGTGAAGTCAACGAGTGCCGAAA
AATTGAGAGTCTTGAAAACCTGTATTTGGATTTTGATGATGATGTACAGAACTTGAAAACCT
TTGGAGTAACCACCACCAAGTATCAAAATCACCAAGTCCAGCAAGTACTTCCACAGTACCT
AACATGACAGATGCTCCTACAGCCCCCAAAGCAGGAACCTACAAGTGTGGCACCAGTGCACC
AGACATTTCTGCTAATTCTAGAAGTTTATCTCAGATTCTGATGGAACAATTGCAAAAGGAGA
AACAGCTGGTCACTGGTATGGATGGTGGCCCTGAGGAATGCAAAAATAAAGATGATCAGGGA
TTTGAATCATGTGAAAAGGTATCAAATTCTGACAAGCCTTTGATACAAGATAGTGACTTGAA
AACATCTGATGCCTTACAGTTAGAAAATCTCAGGAAATTGAACTTCTAATAAAAAATGATA
TGACTATAGATATACTACATGCTGATGGTGAAGACCTAATGTTCTAGAAAACCTAGACAAC
TCAAAGGAAAAGACTGTTGGATCAGAAGCAGCAAAAACCTGAAGATACAGTTCTCTGCAGCAG
TGATACAGATGAGGAGTGTTAATCATTGATACAGAATGTAAAAAAACCAGTTATAACAGTG
TTTAAATTTAGATAAGTTTGAGGGAAAATAATCAGTAGGCAAGAGGAACATTTTTCTGTAGT
AGCTAGAGTGCCTTGAAAAATGTGTTGGCTATGTGAAGGAATATTTCAACTAAAATGGAAT
GGTATGCTTTTACCCCTTAAAGTTTGAGGAGGATCTTGATATGTTTTAACATTATCATGGCA
GGGAAATATATAAAGAAGAAAAATATTTTTACATTAAACCTTTTCTAAAAATTGTAAATAGA
AAAATAATTTGGTTTTTTTATCAAGAACAACACTTATCGTTATGTATTGTGTTAGTTATATTG
CCAGTCTGTTGCGACTGACTCAAAAAGTTAAATGTTGCCACTGCTGAAGATGATTATGAGCA
TCGCAAACCTTTGTTTCTGACCCATTTTGACAGTTTTTATATACTCCTTTAAATGATGAATG
TTACAGGTTAATAAAGTTAATACCTTTAAA

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FIGURE 62

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139540
><subunit 1 of 1, 592 aa, 1 stop
><MW: 66453, pI: 5.42, NX(S/T): 3
MSSKMVISEPGLNWDISPKNGLKTFFSRENYKDHSMAPSLKELRVLSNRRIGENLNASAS
SVENEPAVSSATQAKEKVKTITIGMVLLPKPRVPYPFRSFRSQREQRSYVDLLVKYAKIPA
NSKAVGINKNDYLQYLDMMKKHVNEEVTEFLKFLQNSAKKCAQDYNMLSDDARLFTEKILR
ACIEQVKKYSEFYTLHEVTSLMGFFPFRVEMGLKLEKTLALGSKYVKTVPFSPMPIKLO
LSKDDIATITETSEQTAEAMHYDISKDPNAEKLVSRYHPQIALTSQSLFTLLNNHGPTYKE
QWEIPVCIQVIPVAGSKPVKVIYINSPLPQKKMTMRERNQIFHEVPLKFMMSKNTSVPVS
AVFMDKPEEFISEMDMSCEVNECRKIESLENLYLDFDDDVTELETFGVTTTKVSKSPSPA
STSTVPMNTDAPTAPKAGTTTVAPSAPDISANSRSLSQLMEQLQKEKQLVTGMDGGPEE
CKNKDDQGFESCEKVSNSDKPLIQDSDLKTS DALQLENSQEIETS NKNDMTIDILHADGE
RPNVLENLDNSKEKTVGSEAAKTEDTVLCSSDTDEECLIIDTECKKTSYNSV
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 56-60;354-358;427-431

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 187-191;331-335;585-589

N-myristoylation sites:

Amino acids 126-132;407-413;557-563

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FIGURE 63

TTTTTAACTTGAACTTCCAAGGCCACGTGCGTCTCCTGGCTCCTGCACGGACTGTGTGACTG
TCCCCGACAGCTTTCCTGTCTCGTCTCATGAGGGGTCCAGCACATGGCATTCTGGGTCTGGCA
CCTGAAGTCCACCTCTATGAGACCCTCTGGGAGCGTGACGGGGCCTTGGCATGGGTCTGGCCG
AGGCCCTTCTGTCCCAGGTCACTGGTGTGGTCTGGCCCAGGCCCTCCTGTCCCACATCACCTG
TGTGGTCTGGCCCAGGCCCTCCTGTCCCAGGTCACTGGTGTGGTCTGGCCCAGGCCCTCCTGTC
CAGGTCTCCTGTCCAGGTCACTGGTGTGGTCTGGCCCAGGCCCTTCTGTCCCAGGTCACTG
TGTGGTCTGGCCCAGGCCCTCCTGTACCATGTCACTGTTGAGGGGCTGGCTCTGGAAGAGGG
CAGGGACTTGGCATTGGTGGGGGCAGGGTTCCAAGGTGTGGCCTGTCAGCAGGAAGGGGCAG
GTGGCATGGGTCCAGGCGGGAAGTCAAGGGCTGGGGTGGCACTGCTGGAGACTGTCCGGAGGCC
CCTCCAGGGCACCTTGCCATTGCCATTGTCGCTCATGGCCATCTGGTCCCCTTTCAGGGAAC
AAGAGGAGGATCAGATGCTGCGGGACATGATTGAGAAAGCTGGGTGACTGGGCCGGGGATGCT
GAGGGCTGGGCTGGCTGGCTGGGTGGGCCGGGGATGCTGAGTGCTGGGCTGGCTGGCTGGGT
GGACCGGGCTCCAGCTGGGGGTGGGGGGGGGGCGGGTATCGGGTCCCCCCTCAGCCTTGG
TGACAGGACAGGCAGGTTCAACCCTGAGGGTGAGAGCTCCCTCCCGCCCCCTAAGAGAGCCAGG
GGCAGCTGGTGACCGTGTGGTCATGGTGGGGACAGCCCTCCGGGGCACCCAGTCTGGGGCAG
GTTCTCACGTGGGAGGGCACAGGGCTTCTGTCAGGCTCGGAGGCCAGGGCGGATTGTGGCC
AGTGGAAAGGAAGGATGTTTCTGGCAGGGGGACTTGTGTGGGCCACGGCTGTGCGGCTGCGG
CGTTGAGCACGGCCTCACTGTCCACCTGTCCCCTAGGCCTCCAGAGGAAGAAGTCCAAGTTC
CGCTTGTCCTAAGATCTGGTCACCAAAAAGCAAAAGCAGCCCCTCCCAGTAGTAGCCAGTAGG
GCCGTGGGCTCGGCCCCGGACCTGGCATCCGGACTTGGACTCGGGGCCATGGGCTTGGCCCCG
ACCCGGAACCCGGACTTGTAAGTCTGGGGCCGTGGGCTCGGCCCCGACCCGGCATTCTGGACTTG
GACTCGGGAAGGGCCTCCTGTCCCTACAAGGGGCATGTGGACAGCAGGGACCTGCGCTACCG
TCTGTGGTCTCAATAAAGAAACCGACCACATGGCCCCGGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAACA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139602
><subunit 1 of 1, 159 aa, 1 stop
><MW: 15900, pI: 8.07, NX(S/T): 0
MGRPRPFCPRSLVWSAQALLSHITCVVGPVPGHRCGRPRPSCPGPPVQVTGVVGP GP
SVPGHLCGRPRALLYHVTVEGLALEEGRDLALVGAGFQGVACQQEGAGGMGPGGTQGWGA
TAGDCPEAPPGH LAIAIVAHGHLVFPFQGTRGGS DAAGHD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

N-myristoylation sites:

Amino acids 109-115;113-119;119-125;148-154;151-157;152-158

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FIGURE 65

GGCGACCACCGCCGCTCCTCACCTGGCCATTGGTGCAGCCCGTTCCCGGGCGGCGAGAGAAG
GCAGGGCGGCTCCTTGCGCCACGCCACACCGTCGGGGCCCCCGTCGGGTCCCCCTCGGGCCGCA
ATGGTGGGCTCCGCGCGGCTGGGTCCGGCACTCTTGACCCCTTTGTAACCACCGCGGCGGG
CACCCAGGGAGTTCGAGCAACGAAGTTGGTGACCTGCCCCGCTCCCAGGCAGTTTGCTGTTG
GGGCTTTCACGGCTGCTGGAAGGGCATGGCTGTTTGTCCCATCACTGGGCGCCAGCTTCTCA
AAGCTACGTTACAGCAACGCAGTAGGGACTTTCGTGGCAGGCTTTTTTTAAGAGCTGAAAG
AAGGGCGGGAGGGTTTACGTCC**TAG**GGTGATGATTTCCCTACCAGACAGCGAAGTATCTATT
GGGAAACTCCAGGTGACCGCACCTCCTTCCGACAGTTCGCCCCGGGGCAAGTTTACCAGCTG
CGTCAGAAAGCAGGTTTGCAAAATCCTTGAGAACGGCCTGAGCTAAGGACTGGGGTCAGGA
GGGTTTTAAACTCATCTGATTTTCTTGCAATCATATCTCTTGAAAGTTTTTATATTTTCCC
CAATATTTTTCTGAGTTGCTATATCCAATGAAAAAATGCTGATGTAGAGGTCCACCAGCCA
ATGCTTTATTGGAAGTCAACGAATGAGACCGAGGGTGGCCCATAATCAATCTCGGCACGCGG
GAATGTGAACCTCTTCCAAGGTCTGGGCGAGTCCCTAGAGTTACGCAGATGAAGGACATTGG
CCCTCGAGAATCTCACACCAGCAAAGAAGAGCACAACGAAGCGCAAACACTACTTATGATCATT
GTGGCTTTGGGCAAGTTGTTGTAGCTCCAGCAACAATTTCTTCACCTGGAGTGCAGCAATA
AATGATACTGGTGCTGCAGGGCAGCTAATAAGCTTCTGAATAATATATGCAAAGTACTTGGC
ACCATGAGCAGAACTCAGTATAACCGTCACTGAAGAAATAGCTTATTTAATGATTACACTTTT
CATATGTGCAAGTAAAAGTTTGACTTTTAGGGAGAGCCTCACCTACGGAATGTCTTTTTTAA
ATTTCTTTTTTAATTATACTTTAAGTTCTGGGATACATGTGCAGAACGTGCAGGTTTGTTAC
ACAGGTATACATGTGCCATGGTGGTTTGCAGCACCCATCAACCCTTCATCTAGGTTTTAAGC
TCCGCATGCATTAGTTATTTGTCTAATGCTCTCCCTCCCTTGTCCCCCACCCCCAACAG
GCCTCAGGGTGTGATGTTCCCCCTCCCTGGGTCCATATGTTCTCATTGTTCAACTCCCACTTA
TGATGAGAACATGCAGTGTTTGGTTTTCTGTTCCGTGTGTTAGTTTGCTGAGAATGATGGTTT
CCAGCATCATCCACGTCCCTGCAAAGGACATGAATTCATTCTTTTTTATGGCTGCATGGTAT
TCCATGGTGTATATGTGCCACATTTTCTTCATCCAGTCTATCATTGATGGGCACTTGGGTTG
GTTCCAAGACTTTGTTATTGTGAACAGTGCTGCAATAAACATACGTTTGTATGTGTCAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139632
><subunit 1 of 1, 90 aa, 1 stop
><MW: 9586, pI: 12.18, NX(S/T): 0
MVGSA RLGPALLTPFVTTAAGTQGV RATKLVTCPAPRQFAVGAF TAAGRAWLFVPSLGAS
FSKLRSQQRSRDFRGRLFLRAERRAGGFTS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-myristoylation sites:

Amino acids 24-30;42-48;58-64

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FIGURE 67

CATGTCTAGACTGGGAGCCCTGGGTGGTGCCCGTGCCGGGCTGGGACTGTTGCTGGGTACCG
CCGCCGGCCTTGGATTCTGTGCCTCCTTTACAGCCAGCGATGGAAACGGACCCAGCGTCAT
GGCCGCAGCCAGAGCCTGCCCAACTCCCTGGACTATACGCAGACTTCAGATCCCGGACGCCA
CGTGATGCTCCTGCGGGCTGTCCCAGGTGGGGCTGGAGATGCCTCAGTGCTGCCCAGCCTTC
CACGGGAAGGACAGGAGAAGGTGCTGGACCGCCTGGACTTTGTGCTGACCAGCCTTGTGGCG
CTGCGGCGGGAGGTGGAGGAGCTGAGAAGCAGCCTGCGAGGGCTTGCGGGGGAGATTGTTGG
GGAGGTCCGATGCCACATGGAAGAGAACCAGAGAGTGGCTCGGCGGCGAAGGTTTCCGTTTG
TCCGGGAGAGGAGTGA CTCCACTGGCTCCAGCTCTGTCTACTTCACGGCCTCCTCGGGAGCC
ACGTTACAGATGCTGAGAGTGAAGGGGGTTACACAACAGCCAATGCGGAGTCTGACAATGA
GCGGGACTCTGACAAAGAAAGTGAGGACGGGGAAGATGAAGTGAGCTGTGAGACTGTGAAGA
TGGGGAGAAAGGATTCTCTTGACTTGGAGGAAGAGGCAGCTTCAGGTGCCTCCAGTGCCCTG
GAGGCTGGAGGTTCTCAGGCTTGGAGGATGTGCTGCCCCCTCCTGCAGCAGGCCGACGAGCT
GCACAGGGGTGATGAGCAAGGCAAGCGGGAGGGCTTCCAGCTGCTGCTCAACAACAAGCTGG
TGTATGGAAGCCCGGCAGGACTTTCTCTGGCGCCTGGCCCCGAGCCTACAGTGACATGTGTGAG
CTCACTGAGGAGGTGAGCGAGAAGAAGTCATATGCCCTAGATGGAAAAGAAGAAGCAGAGGC
TGCTCTGGAGAAGGGGGATGAGAGTGCTGACTGTACCTGTGGTATGCGGTGCTTTGTGGTC
AGCTGGCTGAGCATGAGAGCATCCAGAGGCGCATCCAGAGTGGCTTTAGCTTCAAGGAGCAT
GTGGACAAAGCCATTGCTCTCCAGCCAGAAAACCCCATGGCTCACTTTCTTCTTGGCAGGTG
GTGCTATCAGGTCTCTCACCTGAGCTGGCTAGAAAAAAAAACTGCTACAGCCTTGCTTGAAA
GCCCTCTCAGTGCCACTGTGGAAGATGCCCTCCAGAGCTTCCTAAAGGCTGAAGAACTACAG
CCAGGATTTTCCAAAGCAGGAAGGGTATATATTTCCAAGTGCTACAGAGAACTAGGGAAAAA
CTCTGAAGCTAGATGGTGGATGAAGTTGGCCCTGGAGCTGCCAGATGTCACGAAGGAGGATT
TGGCTATCCAGAAGGACCTGGAAGAACTGGAAGTCATTTACGAGACT**TAA**CCACGTTTCACT
GGCCTTCATGACTTGATGCCACTATTTAAGGTGGGGGGGCGGGGAGGCTTTTTTTCCTTAGAC
CTTGCTGAGATCAGGAAACCACACAAATCTGTCTCCTGGGTCTGACTGCTACCCACTACCAC
TCCCCATTAGTTAATTTATTCTAACCTCTAACCTAATCTAGAATTGGGGCAGTACTCATGGC
TTCCGTTTCTGTTGTTCTCTCCCTTGAGTAATCTCTTAAAAAATCAAGATTCACACCTGCC
CCAGGATTACACATGGGTAGAGCCTGCAAGACCTGAGACCTTCCAATTGCTGGTGAGGTGGA
TGAAC TTCAAAGCTATAGGAACAAAGCACATAACTTGTCACTTTAATCTTTTTCACTGACTA
ATAGGACTCAGTACATATAGTCTTAAGATCATACCTTACCTACCAAGGTAAAAAGAGGGATCA
GAGTGGCCACAGACATTGCTTTCTTATCACCTATCATGTGAATTCTACCTGTATTCTTGGG
CTGGACCACTTGATAACTTCCAGTGTCTTGGCAGCTTTTGAATGACAGCAGTGGTATGGGG
TTTATGATGCTATAAAACAATGTCTGAAAAGTTGCCTAGAATATATTTTGTACAAACTTGA
AATAAACCAAATTTGATGTT

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FIGURE 68

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139686
><subunit 1 of 1, 470 aa, 1 stop
><MW: 52118, pI: 5.06, NX(S/T): 0
MSRLGALGGARAGLG LLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG
RHVMLLRVPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG
EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTAN
AESDNERDSKESEDGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGGSSGLEDVLP
LLQQADELHRGDEQKGREGFQLLLNNKLVGSRQDFLWRLARAYSDMCELTEEVSEKKS
YALDGKEEAEEAALEKGDDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAI
ALQPENPMAHFLLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQSFLKAEELQPGF
SKAGRVYISKCYRELGKNSEARWWMKLALELPDVTKEDLAIQKDLEEELEVILRD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 209-213

N-myristoylation sites:Amino acids 5-11;8-14;9-15;15-21;19-25;72-78;164-170;
174-180;222-228;230-236**Amidation sites:**

Amino acids 207-211;254-258

Cell attachment sequence:

Amino acids 250-253

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FIGURE 69

CCCACGCGTCCGAAACACTTTAAACCTGACCAGCTAAATGGATAAACCTAGCCTGCATAGCT
TTTAAACTGGGGTCTCATACAGCACAGGAGGCCTACTTGCTTCAAGAACTGAAAATCCAGAG
GATGAATTGCTTTATCTGGAATGGCAAAGCCAGCACAAATAAGGAATGCCAGTTTGTATGG
GGCTACTAGCTCACATGCGGGATCAGAATGGTGTGAATGACAGCCGCACTGTGTGCATGAAGG
TGGTGGTGGTTTCCGCACAAGAGACCAAATAAGAAGAAAGCTGAGAGAGGGGGGAAACGTTTTT
GGATGACAAAGGATGGGTTTCCATTTAATTACGCAGCTGAAAGGCATGAGTGTGGTGTGGT
GCTACTTCCTACACTGCTGCTTGTATGCTCACGGGTGCTCAGAGAGCTTGCCCAAAGAACT
GCAGATGTGATGGCAAATTTGTGTACTGTGAGTCTCATGCTTTCGCAGATATCCCTGAGAAC
ATTTCTGGAGGGTCACAAGGCTTATCATTAAAGGTTCAACAGCATTGAGAAGCTCAAATCCAA
TCAGTTTGCCGGCCTTAACCAGCTTATATGGCTTTATCTTGACCATAATTACATTAGCTCAGTG
GATGAAGATGCATTTCAAGGGATCCGTAGACTGAAAGAATTAATTCTAAGCTCCAACAAAAT
TACTTATCTGCACAATAAAACATTTACCCAGTTCCCAATCTCCGCAATCTGGACCTCTCCT
ACAATAAGCTTCAGACATTGCAATCTGAACAATTTAAAGGCCTTCGAAACTCATCATTTTG
CACTTGAGATCTAACTCACTAAAGACTGTGCCATAAGAGTTTTTCAAGACTGTGCGAATCT
TGATTTTTTTGGATTTGGGTTACAATCGTCTTCAAGCTTGTCCCGAAATGCATTTGCTGGCC
TCTTGAAGTTAAAGGAGCTCCACCTGGAGCACAAACAGTTTTTCCAAGATCAACTTTGCTCAT
TTTCCACGTCTCTCAACCTCCGCTCAATTTACTTACAATGGAACAGGATTCGCTCCATTAG
CCAAGGTTTGACATGGACTTGGAGTTCTTACACAACCTGGATTTATCAGGGAATGACATCC
AAGGAATTGAGCCGGGCACATTTAAATGCCTCCCCAATTTACAAAATTGAATTTGGATTCC
AACAGCTCACCAATATCTCACAGGAAACTGTCAATGCGTGGATATCATTAATATCCATCAC
ATTGTCTGGAATATGTGGGAATGCAGTCGGAGCATTTGTCCTTTATTTTATTGGCTTAAGA
ATTTCAAAGGAAATAAGGAAAGCACCATGATATGTGCGGGACCTAAGCACATCCAGGGTGAA
AAGGTTAGTGATGCAGTGGAAACATATAATATCTGTTCTGAAGTCCAGGTGGTCAACACAGA
AAGATCACACCTGGTGCCCCAACTCCCCAGAAACCTCTGATTATCCCTAGACCTACCATCT
TCAAACCTGACGTACCCAATCCACCTTTGAAACACCAAGCCCTTCCCCAGGGTTTCAGATT
CCTGGCGCAGAGCAAGAGTATGAGCATGTTTCATTTACAAAATTATTGCCGGGAGTGTGGC
TCTCTTTCTCTCAGTGGCCATGATCCTCTTGGTGATCTATGTGTCTTGGAACGCTACCCAG
CCAGCATGAAACAACCTCCAGCAACACTCTCTTATGAAGAGGCGGCGGAAAAAGGCCAGAGAG
TCTGAAAGACAAATGAATTCCCCTTTACAGGAGTATTATGTGGACTACAAGCCTACAACTC
TGAGACCATGGATATATCGGTTAATGGATCTGGGCCCTGCACATATACCATCTCTGGCTCCA
GGGAATGTGAGATGCCACACCACATGAAGCCCTTGCCATATTACAGCTATGACCAGCCTGTG
ATCGGGTACTGCCAGGCCCCACCAGCCACTCCATGTCACCAAGGGCTATGAGACAGTGTCTCC
AGAGCAGGACGAAAGCCCCGGCCTGGAGCTGGGCGGAGACCACAGCTTCATCGCCACCATCG
CCAGGTCGGCAGCACCGGCCATCTACCTAGAGAGAATTGCAAAC**TAA**CGCTGAAGCCAACTC
CTCACTGGGGAGCTCCATGGGGGGGAGGGAGGGCCTTCATCTTAAAGGAGAATGGGTGTCCA
CAATCGCGCAATCGAGCAAGCTCATCGTTCCTGTTAAACATTTATGGCATAGGGAAAAAAA
AAAAAAAAAAAAA

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142392
><subunit 1 of 1, 590 aa, 1 stop
><MW: 67217, pI: 9.26, NX(S/T): 4
MGFHLITQLKGMSVVLVLLPTLLLVMILTGAQRACPKNCRCDGKIVYCESHAFADIPENIS
GGSQGLSLRFNSIQKLKSNQFAGLNQLIWLYLDHNYISSVDEDAFQGIRRLKELILSSNK
ITYLHNKTFHPVPNLRNLDLSYNKLQTLQSEQFKGLRKLIIHLRSNSLKTVPPIRVFQDC
RNLDFLDLGYNRLRSLSRNAFAGLLKLKELHLEHNQFSKINFAPRLFNLRISIYLQWNR
IRSISQGLTWTWSSLHNLDLSGNDIQGIEPGTFKCLPNLQKLNLDNKLNTNISQETVNAW
ISLISITLSGNMWECSRSICPLFYWLKNFKGNKESTMICAGPKHIQGEKVSDAVETYNIC
SEVQVVNTERSHLVPQTPQKPLIIPRPTIFKPDVTQSTFETPSPSPGFGQIPGAEQEYEHV
SFHKIIAGSVALFLSVAMILLVIYVSWKRYPASMKQLQQHSLMKRRRKKARESERQMNSP
LQEYYVDYKPTNSETMDISVNGSGPCTYTTISGSRECEMPHHMKPLPYYSYDQPVIGYCQA
HQPLHVTGKYETVSPEQDESPGLELGRDHSFIATIARSAAPAIYLERIAN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 425-443

N-glycosylation sites:

Amino acids 58-62;126-130;291-295;501-505

Tyrosine kinase phosphorylation site:

Amino acids 136-143

N-myristoylation sites:Amino acids 29-35;61-67;247-253;267-273;271-277;331-337;
502-508;512-518;562-568**Glycosyl hydrolases family:**

Amino acids 310-319

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FIGURE 71

TTCCAGTCAGAGTTAAGTTAAAACAGAAAAAGGAAGATGGCAAGAATATTGTTACTTTTCC
TCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGAATATTTATGGACCGTCTAGCTTCCAAG
AAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTTCTCTGGCTAGTGCTCAAGAAGATTA
TAATGCCCCGGAAGTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAA
AGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTGGGCTGGCAGTGTTTATGGTGATGGCCAG
GACGAGATGGGAGTCGTGGGTTATTTCCCCAGGAAGTGGTCAAGGAACAGCGTGTGTACCA
GGAAGCTACCAAGGAAGTTCCCACCACGGATATTGACTTCTTCTGCGAGTAATAAATTAGTT
AAAAGTGCAAATAGAAAGAAAACACCAAAAATAAAGAAAAGAGCAAAAGTGGCCAAAAAATG
CATGTCTGTAATTTTGGACTGACGT

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143076
><subunit 1 of 1, 128 aa, 1 stop
><MW: 14332, pI: 4.83, NX(S/T): 0
MARILLLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTISLASAQEDYNAPDCRFINV
KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGGVVGYPFRNLVKEQRVYQEATKEVPT
TDIDFFCE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-14

N-myristoylation site:

Amino acids 84-90

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FIGURE 73

CTCAGATTTGCCATGGAGAAATTTTCAGTCTCGGCAATCCTGCTTCTTGTGGCCATCTCTGG
TACTCTGGCCAAAGACACCACAGTCAAATCTGGATCCAAAAGGACCCAAAGGACTCTCGAC
CCAAACTACCCCAGACCCTGTCCAGAGGTTGGGGAGATCAGCTCATCTGGACTCAGACTTAC
GAAGAAGCCTTATACAAATCCAAGACAAGCAACAGACCCTTGATGGTCATTCATCACTTGGA
CGAATGCCCCGCACAGTCAAGCTTTAAAGAAAGTGTGCTGAAAATAAGGAGATCCAGAAATTG
GCAGAGCAGTTTGTTCCTCAACTTGATCTATGAAACAACGACAAGCACCTTTCTCCTGA
TGGCCAGTACGTCCCCAGAATTGTGTTTGTGGACCCTTCCCTGACGGTGAGGGCAGACATCA
CCGGAAGATACTCAAACCGTCTCTACGCTTATGAACCTTCTGACACAGCTCTGTTGCACGAC
AACATGAAGAAAGCTCTCAAGTTGCTGAAGACAGAGTTGTAGAGTCAACTGTACAGTGCCTC
AGGAGCCGGGAAGGCAGAAGCACTGTGGACCTGCCGATGACATTACAGTTTAATGTTACAAC
AAATGTATTTTTTAAACACCCACGTGTGGGGAAACAATATTATTATCTACTACAGACACATG
ATTTTCTAGAAAATAAAGTCTTGTGAGAACTCCAAA

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FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143294
><subunit 1 of 1, 175 aa, 1 stop, 1 unknown
><MW: 19888.97, pI: 9.08, NX(S/T): 0
MEKFSVSAILLLLVAISGTLAKDTTVKSGSKKDPKDSRPKLPQTL SRGWGDQLIWTQTYEE
ALYKSKTSNRPLMVIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLIYETTDKHLSP
DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALLHDNMKKALKLLKTEL
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

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FIGURE 75

GCCGGCGCCAGGGCAGGCGGGCGGCTGGCAGCTGTGGCGCCGAC**ATGGCT**GCGCTGGTGGAG
CCGCTGGGGCTGGAGCGGGACGTGTCCCGGGCGGTTGAGCTCCTCGAGCGGCTCCAGCGCAG
CGGGGAGCTGCCGCCGCAGAAGCTGCAGGCCCTCCAGCGAGTTCTGCAGAGCCGCTTCTGCT
CCGCTATCCGAGAGGTGTATGAGCAGCTTTATGACACGCTGGACATCACCGGCAGCGCCGAG
ATCCGAGCCCATGCCACAGCCAAGGCCACAGTGGCTGCCTTCACAGCCAGCGAGGGCCACGC
ACATCCCAGGGTAGTGGAGCTACCCAAGACGGATGAGGGCCTAGGCTTCAACATCATGGGTG
GCAAAGAGCAAACTCGCCCATCTACATCTCCCGGGTCATCCCAGGGGGTGTGGCTGACCGC
CATGGAGGCCTCAAGCGTGGGGATCAACTGTTGTGGTGAACGGTGTGAGCGTTGAGGGTGA
GCAGCATGAGAAGGCGGTGGAGCTGCTGAAGGCGGCCAGGGCTCGGTGAAGCTGGTTGTCC
GTTACACACCGCGAGTGCTGGAGGAGATGGAGGCCCGGTTGAGAAGATGCGCTCTGCCCGC
CGGCGCCAACAGCATCAGAGCTACTCGTCCTTGGAGTCTCGAGGT**TGA**AACACAGATCTGG
ACGTTACGTGCACTCTCTCCTGTACAGTATTTATTGTTTCCTGGCACTTTATTAAAGATA
TTTGACCCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143514
><subunit 1 of 1, 207 aa, 1 stop
><MW: 22896, pI: 8.93, NX(S/T): 0
MAALVEPLGLERDVSRAVELLERLQSGELPPQKLQALQRVLQSRFCSAIREVYEQLYDT
LDITGSAEIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIYIS
RVIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVLEE
MEARFEKMRSARRRQQHQSYSSLESRG
```

Tyrosine kinase phosphorylation site:

Amino acids 51-59

N-myristoylation sites:

Amino acids 102-108;133-139

Cell attachment sequence:

Amino acids 136-139

PDZ domain (Also known as DHR or GLGF):

Amino acids 93-174

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144841
><subunit 1 of 1, 208 aa, 1 stop
><MW: 22187, pI: 5.08, NX(S/T): 1
MDSDETGFHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHL
EIREDDGTVGGAADQSPESLLQLKALKPGVILGVKTSRFLCQRPDGALYGSLHFDPEAC
SFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGIL
APQPPDVGSSDPLSMVGPSQGRSPSYAS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-myristoylation sites:

Amino acids 12-18;20-26;23-29;66-72;94-100;107-113;168-174

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 15-26

HBGF/FGF family proteins:

Amino acids 57-73;80-131

FIGURE 79

[illegible]

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FIGURE 80

Protein File:

MW: 73502.97, pI: 9.26

MSSQPAGNQTS PGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLS
ILVLLLLLAMLVRRRQLWPD CVRGRPLSPVDFLAGDRPRVPAAVFMVLLSSLCLLLPD
EDALPFLTLASAPSQDGKTEAPRGAWKILGLFYAAALYYPLAACATAGHTAAHLLGSTLS
WAHLGVQVWQRAECPQVPKIYKYISLLASLPLLLGLGFLSLWYPVQLVRSFSSRTGAGSK
GLQSSYSEEYLRNLLCRKKLGSSYHTSKHGFSLSWARVCLRHCIYTPQPGFHLPLKLVLSA
TLTGTAIYQVALLLLVGVVPTIQKVRAGVTTDVS YLLAGFGIVLSEDKQEVVELVKHHLW
ALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI FCW
MSFSAYQTAFICLGLLVQQIIFFLGTTALAFVLMPVLHGRNLLLFRSLESSWPFWLT LA
LAVILQNMAAHWVFLETHDGHQPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYN
AIHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA
APQDSL RPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALL
GANGAQP

Important features of the protein:**Transmembrane domains:**

Amino acids 54-69;102-119;148-166;207-222;301-320;
364-380;431-451;474-489;512-531

N-glycosylation site:

Amino acids 8-12

N-myristoylation sites:

Amino acids 50-56;176-182;241-247;317-323;341-347;525-531;
627-633;631-637;640-646;661-667

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 364-375

ATP/GTP-binding site motif A (P-loop):

Amino acids 132-140

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FIGURE 81

AAAAAATACAGCAGGTGAAGGAGGTTGGAGAGTAGGGGGTGGAGGGCCACGCAGCACTTGT
CCTTCACCCTGGAGGGGATCTGTTACATGCCCCAGATTGCTGGTCCCCTAGAAATGTTACTG
AGGCAGCCTCTGCATTTTTGCAGGGATTGTTTTCTACTGTTTGACATTACGTAACCTCCTA
ACGCTGTCTGGGGAAGATGCTACCCCCTGCTCTCCCCGTCTTTCCTGCACTCTCAGCAATGG
GATGGGCTGACTGATGCCCTGTGGGCTGGAAAGCTGACCACAGTTGCTGCAGACCAGACCCC
CTCACATAGTGAGTGCTGGGCTGAGGAATCCAGGAGAGCCCGAGGGGGGACACTGAAGGTGT
ATCGTTGGCCCTGCCAGCTGCAAGTGAAGTCTTCTGATGAATTTTAATAGGGAGAAAGAAG
TATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATC
AATATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGAAACATGACCAAGATTGGGCAA
ACGTCTCCAACATGACTTTTCAGCAACGGAAACTAAGAGTCAAAGGCATTTATTACCGGAAT
GCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT
ATGGTGTAATTTGAGGTCAGTGGCCAGAGGACAGATCCCGTCTACATTATTGAGTGAAGCGGAGA
GCTACTGCAGGGTTCTGAGCAGAGTCCTAATTTATATTTTAGAAGAATCATCATGGCTCCTA
GATTAGGAATAAAACGAAGGGGCCAGGGATGGAAACGATGAGTCCAGTTGGGTACTGCAA
AGATCCAGGCCAGAAATCCAGGCACAGTGGCACACACCTGAGTCCCAGATAATTCCACCTAC
TGGTCCTGCTCTGTGGCCTACTGGTCCGAGTCCAGCCCCGACTGATTTCTGGGCCTGTAATG
TCTAAAAACGCTCCCTGCTGATGTTTTGCAAGTGAAGTGTGTTACTTGAAGGCAGTTCCTAGG
ATAAACTAGTCGCTTTATCATTACAGAATCATTCAGTGAAGCATCAACTATGTAACCAGCATT
GGGTGGGTGCCAGAGATCCAAAGCTAAGACACCAAACCTGCTCTCCAGGAAACGAGAGGC
TGAGAA

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FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149995
><subunit 1 of 1, 95 aa, 1 stop
><MW: 10704, pI: 10.00, NX(S/T): 2
MAILTSLQLILLIPSLISHEAHKTSLSWKHDQDWANVSNMTFSGKLRVKGIYYRNAD
ICSRHRVTSAGLTLDLQLWCNLRVARGQIPSTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

N-glycosylation sites:

Amino acids 38-42;41-45

N-myristoylation site:

Amino acids 89-95

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FIGURE 83

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCGGCTGACTGCGCCTCTGCTT
TCTTTCCATAACCTTTTCTTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTCCGGA
CACTAGGGTGCCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAACCA**ATG**CT
GCCGCCGCCGCGGCCCGCAGCTGCCTTGGCGCTGCCTGTGCTCCTGCTACTGCTGGTGGTGC
TGACGCCGCCCCCGACCGGCGCAAGGCCATCCCCAGGGCCAGATTACCTGCGGCGCGGCTGG
ATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGAGTGCGCCGCGCC
GCGGGGCTGCCTGGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTGGGAATGCGCCAACC
TCGAGGGCCAGCTCTGCGACCTGGACCCAGTGCTCACTTCTACGGGCACTGCGGCGAGCAG
CTTGAGTGCCGGCTGGACACAGGCGGGCAGCTGAGCCGCGGAGAGGTGCCGGAACCTCTGTG
TGCTTGTGCTTCGCAGAGTCCGCTCTGCGGGTCCGACGGTACACCTACTCCAGATCTGCC
GCCTGCAGGAGCGGCCCCGCGCTCGGCCCCGATGCCAACCTCACTGTGGCACACCCGGGGCCC
TGCGAATCGGGGCCCCAGATCGTGTACATCCATATGACACTTGGAATGTGACAGGGCAGGA
TGTGATCTTTGGCTGTGAAGTGTTTGCCTACCCCATGGCCTCCATCGAGTGGAGGAAGGATG
GCTTGGACATCCAGCTGCCAGGGGATGACCCCCACATCTCTGTGCAGTTTAGGGGTGGACCC
CAGAGGTTTGAGGTGACTGGCTGGCTGCAGATCCAGGCTGTGCGTCCCAGTGATGAGGGCAC
TTACCGCTGCCTTGGCCGCAATGCCCTGGGTCAAGTGGAGGGCCCTGCTAGCTTGACAGTGC
TCACACCTGACCAGCTGAACTCTACAGGCATCCCCCAGCTGCGATCACTAAACCTGGTTCCCT
GAGGAGGAGGCTGAGAGTGAAGAGAATGACGATTACTACT**TAG**GTCCAGAGCTCTGGCCCATG
GGGTGGGTGAGCGGCTATAGTGTTTCATCCCTGCTCTTGAAAAGACCTGGAAAGGGGAGCAG
GGTCCCTTCATCGACTGCTTTTCATGCTGTGTCAGTAGGGATGATCATGGGAGGCCTATTTGACT
CCAAGGTAGCAGTGTTGGTAGGATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAG
ACCAGGACCGGTGGGGTACAAAGGGGCCCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCA
ACAGGTTGTTTCCCAGGCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGAT
TCTCCACTTCTTCCAGCCCTGCTGGGCCACAGTTCTAACTGCCCTTCTCCCAGGCCCTGGT
TCTTGCTATTTCCCTGGTCCCCAACGTTTATCTAGCTTGTTTGGCCTTTCCCCAACTCATCT
TCCAGAACTTTTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAACTGCAGTCCCTTTTGCT
GTCTGCCGTCTTTTGTACAAGAGAGAGAACAGCGGAGCATGACTTAGTTTCACTGCAGAGAGA
TTT

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FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA167678
><subunit 1 of 1, 304 aa, 1 stop
><MW: 32945, pI: 4.69, NX(S/T): 3
MLPPPRPAAALALPVLLLLLVLTTPPTGARPSPGPDYLRRGWMRLLAEGEGCAPCRPEE
CAAPRGCLAGRVRDAGCCWECANLEGQLCDLDP SAHFYGHCGEQLECRDGTGGDL SRGE
VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTV AHPGPCESGPQIVSHPYD
TWNVTGQDVI FGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTCWLQI
QAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVP EEEAESEEN
DDYY
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 159-163;183-187;277-281

Tyrosine kinase phosphorylation site:

Amino acids 244-252

N-myristoylation sites:

Amino acids 52-58;66-72;113-119;249-255

Kazal-type serine protease inhibitor domain:

Amino acids 121-168

Immunoglobulin domain:

Amino acids 186-255

Insulin-like growth factor binding proteins:

Amino acids 53-90

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FIGURE 85

CAAAGCGGCGGCTGTCCGCGGTGCCGGCTGGGGGCGGAGAGGCGGCGGTGGGCTCCCTGGGG
TGTGTGAGCCCGGTGATGGAGCCGGGCCCCGACAGCCGCGCAGCGGAGGTGTTGCTTGCCGCC
GTGGCTGCCGCTGGGGCTGCTGCTGTGGTGGGGCTGGCCCTGGGCGCGCTCCCCTTCGGCA
GCAGTCCGCACAGGGTCTTCCACGACCTCCTGTGCGAGCAGCAGTTGCTGGAGGTGGAGGAC
TTGTCCCTGTCCCTCCTGCAGGGTGGAGGGCTGGGGCCTCTGTGCTGCCCCGGACCTGCC
GGATCTGGATCCTGAGTGCCGGGAGCTCCTGCTGGACTTCGCCAACAGCAGCGCAGAGCTGA
CAGGGTGTCTGGTGCGCAGCGCCCGGCCCGTGCGCCTCTGTCAGACCTGCTACCCCTCTTC
CAACAGGTCGTCAGCAAGATGGACAACATCAGCCGAGCCGCGGGGAATACTTCAGAGAGTCAG
AGTTGTGCCAGAAGTCTCTTAATGGCAGATAGAATGCAAATAGTTGTGATTCTCTCAGAATT
TTTTAATACCACATGGCAGGAGGCAAATTGTGCAAATTGTTTAACAAACAACAGTGAAGAAT
TATCAAACAGCACAGTATATTTCCCTTAATCTATTTAATCACACCCTGACCTGCTTTGAACAT
AACCTTCAGGGGAATGCACATAGTCTTTTACAGACAAAAATTATTCAGAAGTATGCAAAAA
CTGCCGTGAAGCATACAAAACCTCTGAGTAGTCTGTACAGTGAAATGCAAAAAATGAATGAAC
TTGAGAATAAGGCTGAACCTGGAACACATTTATGCATTGATGTGGAAGATGCAATGAACATC
ACTCGAAAACCTATGGAGTCGAACTTTCAACTGTTCACTCCCTTGCAGTGACACAGTGCCTGT
AATTGCTGTTTCTGTGTTTCTCTTTCTACCTGTTGTCTTCTACCTTAGTAGCTTTCTTC
ACTCAGAGCAAAAGAAACGCAAACTCATTCTGCCCAAACGTCTCAAGTCCAGTACCAGTTTT
GCAAAATATTCAGGAAAATTCAAACTGAGACCTACAAAATGGAGAATTGACATATCACGTGAA
TGAATGGTGAAGACACAACCTTGGTTTCAGAAAGAAGATAAACTGTGATTTGACAAAGTCAAG
CTCTTAAGAAATACAAGGACTTCAGATCCATTTTTTAATAAGAATTTTCGATTTTCTTTCC
TTTTCCACTTCTTTCTAACAGATTGGATATTTTTTAATTTCCAG

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FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA168028
><subunit 1 of 1, 334 aa, 1 stop
><MW: 37257, pI: 5.95, NX(S/T): 10
MEPGPTAAQRRCSLPPWLPLGLLLWSGLALGALPFGSSPHRVFHDLLSEQQLLEVEDLSL
SLLQGGGLGPLSLPPDLPLDPECRELLLDFASSAELTGCLVRSARPVRLCQTCYPLFQ
QVVS KMDNISRAAGNTSESQSCARSLLMADRMQIVVILSEFFNTTWQEANCANCLTNNSE
ELSNSTVYFLNLFNHTLTTCFEHNLQGNAHSLLOTKNYSEVCKNCREAYKTLSSSLYSEMOK
MNELENKAEPGTHLCIDVEDAMNITRKLWSRTFNCSVPCSDTVPVIAVSVFILFLPVVFY
LSSFLHSEQKKRKLILPKRLKSSTSFANIQENSN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-31

Transmembrane domain:

Amino acids 278-300

N-glycosylation sites:Amino acids 93-97;128-132;135-139;163-167;177-181;
184-188;194-198;216-220;263-267;274-278**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 10-14

N-myristoylation sites:

Amino acids 27-33;206-212;251-257

Leucine zipper pattern:

Amino acids 190-212

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FIGURE 87

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCAGGGC
GGGCAGGCGCCCCGCGCGGGCCGCGGGGCTGCGCGGACCGCCGGAGGAGCTACTGGAGCAGC
TGTACGGGCGCCTGGCGGCCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCG
CGTGAGCAGGCGCGCAACGCGAGCTGCCCCGGCAGGGGGCAGGCCCCGCGACCGCCGCTTCCG
GCCGCCACCAACCTGCGCAGCGTGTGCCCCTGGGCCTACAGAATCTCCTACGACCCGGCGA
GGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTT
GGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCGTGTCTACATGCCACCGTCGTCCTGCGCCG
CACCCCCGCTGCGCCGGCGGGCCGTTCCTGTCTACACCGAGGCCTACGTACCATCCCCGTGG
GCTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAA
CAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCCGCTGGCCCC**TG**AGGCCCGGTCTTG
CCCCGGGAGGTCTCCCCGGCCCGCATCCCGAGGCGCCCCAAGCTGGAGCCGCTGGAGGGCTC
GGTCGGCGACCTCTGAAGAGAGTGCACCGAGCAAACCAAGTGCCGGAGCACCAGCGCCGCT
TTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCATCCCTGGCTTGCTTTTAGCTAC
AAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGGGCATCCTGTGTGCGGC
CCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATCGGCTGCT
GCGGGTGCAGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTT
TTAAAGCAATCTAAAAATAATAATAAGTATAGCGACTATATACCTACTTTTAAATCAACTG
TTTTGAATAGAGGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTA
ACATATAAACATCGTTTTTTTACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTT
GGATAAATTTTGTAGCTGGTACACTCTGGCCTGGGTCTCTGAATTCAGCCTGTACCCGATGG
CTGACTGATGAAATGGACACGTCTCATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACG
GGCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGT
TCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGCACAAAT
TTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGT
GGAACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGG
GCTTTAGGATCAGGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAAT
CTGGAGGCTTCTGTTTCTGCATTCTGCCACGAGAGCTAGGTCTTGATCTTTCTTTAGATT
GAAAGTCTGTCTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTTTAAATCATTAAA
AGAGGCTTGCTGAAGGAT

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FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA173894
><subunit 1 of 1, 202 aa, 1 stop
><MW: 21879, pI: 9.30, NX(S/T): 2
MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQL
GPREQARNASCPAGGRPGDRFRPPTNLRVSPWAYRISYDPARYPRYLPEAYCLCRGCL
TGLFGCEEDVRFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI
NSSIDKQGAKLLLGPNDAPAGP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 68-72;181-185

Tyrosine kinase phosphorylation site:

Amino acids 97-106

N-myristoylation sites:

Amino acids 17-23;49-55;74-80;118-124

Amidation site:

Amino acids 21-25

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FIGURE 89

CCGGGGCCTCCGGAGAACGCTGTCCCATGAACGTGCGGGGAGCGGCCCGCGCTCCGCGCG
TCCCCGCGTCCCTGGCAATTCCCGACTTCCCAACGGCTTCCCGCTGGCAGCCCCGAAGCCGC
ACC**ATG**TTCGCGCTCTGGTTGCTGCTGGCCGGGCTCTGCGGCCTCCTGCGCTCAAGACCCGGT
TTTCAAATTCACCTTCTACAGATCGTAATTCCAGAGAAAATCAAACAAATACAAATGACAG
TTCAGAAATAGAATATGAACAAATATCCTATATTATTCCAATAGATGAGAACTGTACACTG
TGCACCTTAAACAAAGATATTTTTTAGCAGATAATTTTATGATCTATTTGTACAATCAAGGA
TCTATGAATACTTATTCTTCAGATATTCACTCAATGCTACTATCAAGGAAATATTGAAGG
ATATCCAGATTCCATGGTCACACTCAGCACGTGCTCTGGACTAAGAGGAATACTGCAATTTG
AAAATGTTTCTTATGGAATTGAGCCTCTGGAATCTGCAGTTGAATTTCAAGCATGTTCTTTAC
AAATTAAAGAATGAAGACAATGATATTGCAATTTTTATTGACAGAAGCCTGAAAGAACAACC
AATGGATGACAACATTTTTATAAGTGAAAAATCAGAACCAGCTGTTCCAGATTTATTTCCCTC
TTTATCTAGAAATGCATATTGTGGTGGACAAAACTTTGTATGATTACTGGGGCTCTGATAGC
ATGATAGTAACAAATAAAGTCATCGAAATTGTTGGCCTTGCAAATTCATGTTCCACCAATT
TAAAGTTACTATTGTGCTGTCATCATTGGAGTTATGGTCAGATGAAAAAAGATTTCTACAG
TTGGTGAGGCAGATGAATTATTGCAAAAATTTTAGAATGGAAACAATCTTATCTTAACCTA
AGGCCCTCATGATATTGCATATCTACTAATTTATATGGATTATCCTCGTTATTTGGGAGCAGT
GTTTCTGGAACAATGTGTATTACTCGTTATTCTGCAGGAGTTGCATTGTACCCCAAGGAGA
TAACTCTGGAGGCATTTGCAGTTATTGTCAACCAGATGCTGGCACTCAGTCTGGGAATATCA
TATGACGACCCAAAGAAATGTCAATGTTTCAAGATCCACCTGTATAATGAATCCAGAAGTTGT
GCAATCCAATGGTGTGAAGACTTTTAGCAGTTGCAGTTTGAGGAGCTTCAAATTTCAATTT
CAAATGTGGGTGTCAAATGTCTTCAGAATAAGCCACAAATGCAAAAAAATCTCCGAAACCA
GTCTGTGGCAATGGCAGATTGGAGGGAAATGAAATCTGTGATTGTGGTACTGAGGCTCAATG
TGGACCTGCAAGCTGTTGTGATTTTCGAACCTGTGTACTGAAAGACGGAGCAAATGTTATA
AAGGACTGTGCTGCAAAGACTGTCAAATTTACAATCAGGCGTTGAATGTAGGCCGAAAGCA
CATCCTGAATGTGACATCGCTGAAAATTGTAATGGAAGCTCACCAGAATGTGGTCTGACAT
AACTTTAATCAATGGACTTTTCATGCAAAAATAATAAGTTTATTTGTTATGACGGAGACTGCC
ATGATCTCGATGCACGTTGTGAGAGTGTATTTGGAAAAGGTTCAAGAAATGCTCCATTTGCC
TGCTATGAAGAAATACAATCTCAATCAGACAGATTTGGGAAGTGTGGTAGGGATAGAAATAA
CAAATATGTGTTCTGTGGATGGAGGAATCTTATATGTGGAAGATTAGTTTGTACCTACCCTA
CTCGAAAGCCTTTCCATCAAGAAAATGGTGATGTGATTTATGCTTTTCGTACGAGATTCTGTA
TGCATAACTGTAGACTACAAATTGCCTCGAACAGTTCCAGATCCACTGGCTGTCAAAAATGG
CTCTCAGTGTGATATTGGGAGGGTTTGTGTAAATCGTGAATGTGTAGAATCAAGGATAATTAAG
GCTTCAGCACATGTTTGTTCACAACAGTGTCTGGACATGGAGTGTGTGATTCCAGAAACAA
GTGCCATTGTTTCGCCAGGCTATAAGCCTCCAAACTGCCAAATACGTTCCAAAGGATTTTCCA
TATTTCTGAGGAAGATATGGGTTCATCATGGAAAGAGCATCTGGGAAGACTGAAAACACC
TGGCTTCTAGGTTTCTCATTGCTCTTCTCATTGTAACAACCGCAATAGTTTGGC
AAGGAAACAGTTGAAAAAGTGGTTCGCCAAGGAAGAGGAATCCCAAGTAGCGAATCTAAAT
CGGAAGGTAGCACACAGACATATGCCAGCCAATCCAGCTCAGAAGGCAGCACTCAGACATAT
GCCAGCCAAACCAGATCAGAAAGCAGCAGTCAAGCTGATACTAGCAAATCCAAATCAGAAGA
TAGTGCTGAAGCATATACTAGCAGATCCAAATCACAGGACAGTACCCAAACACAAAGCAGTA
GTAAC**TAG**TGATTCCTTCAGAAGGCAACGGATAACATCGAGAGTCTCGCTAAGAAATGAAAA
TTCTGTCTTTCTTCCGTGGTCACAGCTGAAAGAAACAATAAATTGAGTGTGGATC

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FIGURE 90

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA176775
><subunit 1 of 1, 787 aa, 1 stop
><MW: 87934, pI: 5.49, NX(S/T): 4
MFRLWLLLAGLCGLLASRPGFQNSLLQIVPEKIQNTNTDSSEIEYEQISYIIPIDEKLY
TVHLKQRYFLADNFMIIYLYNQGSMTYSSDIQTQCYQGNIEGYPDSMVTLSTCSGLRGI
LQFENVSYGIEPLESAVEFQHVLYKLKKNEDNDIAIFIDRSLKEQPMDDNIFISEKSEPAV
PDLFPLYLEMHIVVDKTLTYDWGSDSMIVTNKVIEIVGLANSMTQFKVTIVLSSLELWS
DENKISTVGEADELLQKFLEWKQSYLNLRPHDIAYLLIYMDYPRYLGAFFPGTMCITRYS
AGVALYPKEITLEAFAVIVTQMLALSLGISYDDPKKCQCSESTCIMNPEVVQSNQVKTFS
SCSLRSFQNFISNVGVKCLQNKPMQKSPKPVCGNGRLEGNEICDCGTEAQCGPASCCD
FRTCVLKDGAKCYKGLCKDCQILQSGVECRPKAHPECDIAENCNGSSPECQPDITLING
LSCKNNKFICYDGDCHDLARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNNKYV
FCGWRNLICGRLVCTYPTKPFHQENGDIYAFVRDSVCITVDYKLPRTVPDPLAVKNGS
QCDIGRVCVNRECVESRIIKASAHVCSQQCSGHGVCDSRNKCHCSPGYKPPNCQIRSKGF
SIFPEEDMGSIMERASGKTENTWLLGFLIALPILIVTTAIVLARKQLKKWFAKEEEFPSS
ESKSEGSTQTYASQSSSEGSTQTYASQTRSESSSQADTSKSKSEDSAEAYTSRSKSQDST
QTQSSSN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 309-326;681-705

N-glycosylation sites:

Amino acids 39-43;125-129;465-469;598-602

Glycosaminoglycan attachment site:

Amino acids 631-635

Tyrosine kinase phosphorylation site:

Amino acids 269-276

N-myristoylation sites:Amino acids 13-19;82-88;99-105;218-224;401-407;634-640;
726-732;739-745**EGF-like domain proteins:**

Amino acids 642-654

Disintegrins proteins:

Amino acids 400-407;422-472;403-453;467-517;634-684

Reprolysin (M12B) family zinc metalloprotease:

Amino acids 186-383

Reprolysin family propeptide:

Amino acids 63-176

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FIGURE 91

CACCAGACAGCACTCCAGCACTCTGTTTGGGGGGCATTTCGAAACAGCAAAATCACTCATAAA
AGGCCAAAAAATTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGAAAAG
ACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTGAGCTTGTTCCACCTCAG
CTGGGAATGTCATCAGGCAACTCAAGTTTTTACCACGGCATGTGTCTGTGAATGTCCGCA
AAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGG
ATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTT
CTGTGTCTACTACTATAGGAAAAATTTAACCTGCACCTGGAGTCCAGGAAAGGAAACCAGTT
ATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACAACC
AATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTCTTCCAAGAATAACGATCCC
AGATAATTATACCATTTGAGGTGGAAGCTGAAAATGGAGATGGTGTAAATTAATCTCATATGA
CATACTGGAGATTAGAGAACATAGCGAAAACCTGAACCACCTAAGATTTTCCGTGTGAAACCA
GTTTTGGGCATCAAACGAATGATTCAAATTGAATGATAAAGCCTGAGTTGGCGCCTGTTTC
ATCTGATTTAAAATACACACTTCGATTACAGGACAGTCAACAGTACCAGCTGGATGGAAGTCA
ACTTCGCTAAGAACCGTAAGGATAAAAACCAAACGTACAACCTCACGGGGCTGCAGCCTTTT
ACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGTCAAAGTTCTGGAGTGAAGTGGAG
CCAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCCATGTGGCCTGGAAGTGTGGAGAGTCC
TGAAACCAGCTGAGGCGGATGGAAGAAGGCCAGTGCGGTTGTTATGGAAGAAGGCAAGAGGA
GCCCCAGTCCTAGAGAAAACACTTGGCTACAACATATGGTACTATCCAGAAAAGCAACACTAA
CCTCACAGAAACAATGAACACTACTAACCAGCAGCTTGAAGTGCATCTGGGAGGCGAGAGCT
TTTGGGTGTCTATGATTTCTTATAATTCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATT
CCAGCTATTCAAGAAAAATCATTTCAAGTGCATTGAGGTGATGCAGGCCTGCGTTGCTGAGGA
CCAGCTAGTGGTGAAGTGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGT
TTCCGGATGTGGACTCAGAGCCCACCACCTTTCTGGGAATCTGTGTCTCAGGCCACGAAC
TGGACGATCCAGCAAGATAAATTAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAAT
GTTGCATGACAAAGTTGGCGAGCCATATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCAT
CAGAAGGTCCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAA
GAGATTCCCAAGAGTGAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGA
AGGTGGAAAAGGATTCTGTAAGCACGCCCATAGCGAAGTGGAAGGAAAGGCAAGGCAAGGCA
TAGATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCATCTCATTGTGACTTGCAACCT
GGCATGAATCACTTAGCTTCTTTAAATCTCTGAAAATGGGGCCAAGAGCACCCACCTTTT
GGGGTTTGGGGGTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGATCCTGAGGAAAT
GGAAGGAGTTGTTATAATTTGTCTTGGTTAGGCCCTGAATTGACCTCCCGGAGCTCCCCGA
CCATCATTTCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCCTGTACACCA
TGACTTCTACTGCCCTGCCAAATCATGCTTTTGTGTTTTTTCAGTCCACCTTATCTCCTGACATCT
TAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTTCTTATGGTAAAATA
CACGTAAAATATTTTTCCAGTTTAAACATTTGAAAGTGTACAATTTAGTGGCATTAGAAGCA
TTCACAATATTGTGCAACCATCACCCTATTTCCAGAACTCTTCTATTTCTGCCCAAATAGA
AGCCCTATACCCATTCAATAGTCACTCCCCATTCCTCTCCTCCCACAGCCCCCTGGCAACTAC
CAAACGTCTTTGTGTCTCTATGGATTGCCTATTTTGGATATTTTCATATACATAGAATCATAA
ANTAAAAA

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FIGURE 92

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA177313
><subunit 1 of 1, 582 aa, 1 stop
><MW: 66605, pI: 8.14, NX(S/T): 15
MCIRQLKFFTTACVCECPQNILSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENI
SCVYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTNSSTSENRASCSFFLPRI
TIPDNYTIEVEAENG DGVKSHMTYWRL ENIAKTEPPKIFRVKPVLG IKRMIQIEWIKPE
LAPVSSDLKYTLRFRTVNSTSWMEVNF AKNRKDKNQTYNLTGLQPFTEYVIALRC AVKES
KFWSDWSQEKMGMT EEEAPCGLELW RVLPKPAEADGRRPVRL LWKKARGAPVLEKTLG YNI
WYYPESNTNLTETMNTTNQQLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQC
IEVMQACVAEDQLVVWKQSSALDVNTWMIEWFPD VDSEPTTLSWESVSQATNWTIQQDKL
KPFWCYNISVYPMLHDKVGE PYSIQAYAKEGVPSEGPETKVENIGVKT VITWKEIPKSE
RKGIIICNYTIFYQAEGGKG FCKHAHSEVEKNPKPQIDAMDRPVVGM APPSHCDLQPGMNH
LASLNLSENGAKSTHLLGFWGLNESEVTV PERRVLRKWKELL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:Amino acids 59-63;69-73;99-103;103-107;125-129;198-202;
215-219;219-223;309-313;315-319;412-416;
427-431;487-491;545-549;563-567**N-myristoylation sites:**

Amino acids 32-38;137-143;483-489;550-556;561-567

Amidation site:

Amino acids 274-278

Growth factor and cytokines receptors family signature 1:

Amino acids 62-75

Fibronectin type III domain:

Amino acids 54-144;154-247

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FIGURE 93

ATTCTCCTAGAGCATCTTTGGAAGC**ATG**AGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCCTGTACCC**TAA**AAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

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FIGURE 94

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57700
<subunit 1 of 1, 125 aa, 1 stop
<MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAI
LSLKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSTRNRR
HVLYP

Important features:**Signal peptide:**

Amino acids 1-21

N-myristoylation sites:

Amino acids 33-39;70-76

Anaphylatoxin domain proteins:

Amino acids 50-60

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FIGURE 95

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGCTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCCTGTGATTTT
ATCCAACCTACTTACCTTGCCTACGATATCCCCTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 96

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62872
<subunit 1 of 1, 90 aa, 1 stop
<MW: 9039, pI: 4.37, NX(S/T): 1
MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPT
ATTAASTTARKDIPVLPKWVGDL PNGRVCP

Important features:**Signal peptide:**

Amino acids 1-19

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FIGURE 97

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**ACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 98

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62876
<subunit 1 of 1, 120 aa, 1 stop
<MW: 12925, pI: 9.46, NX(S/T): 0
MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGR
AGGGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

Important features:**Signal peptide:**

Amino acids 1-17

N-myristoylation sites:

Amino acids 58-64;63-69;64-70;83-89;111-117;115-121

FIGURE 99

[illegible]

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FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66660
><subunit 1 of 1, 209 aa, 1 stop
><MW: 21588, pI: 5.50, NX(S/T): 0
MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQOQSNQVFPSLSLIPLTQML
TLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQOQLHPHVLPIFVTQLGAQGTILSSEELP
QIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSGTTD
DFAVTTPAGIQRSTHAIEEATTESANGIQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Leucine zipper patterns:

Amino acids 10-32;17-39

N-myristoylation sites:Amino acids 12-18;25-31;36-42;74-80;108-114;111-117;
135-141;151-157;159-165;166-172;189-195

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FIGURE 101

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCACTGGGCGTCTTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCACTATTAGAGGTCCCACCCCAAACCTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATCGGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCCTTTATACAATG

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FIGURE 102

MITGVFSMRLWTFVGVLTSLAYCLHQRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQV
EWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIP
FLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPPIIHTDEADSEVLYPNYQSCWSLRQRTGRRQTA
SLQPGISEDLLKKVKDRMGIDSSDKVDFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRES
LQMAVGPFLLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESK
EWFVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 103

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCCGA
CCCCCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCGGCTCCCTGCGCCGCGCGCCGCTC
CCGGGACAGAAGATGCTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCTGCA
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACAGCCACAGTGCCCAACCA
CGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGCGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCCCAACGCCACTTACTCCGTCTGTGTATGCCCTTGGGGCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAGGGAGTGAAGGTC
CCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGCTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCAGAGTGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCATTTATCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
ATAAAAAAAAAA

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FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V F P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

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FIGURE 105

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

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FIGURE 106

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHF
WGKGCCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:**Signal peptide:**

Amino acids 1-20

N-glycosylation site:

Amino acids 72-76

Tyrosine kinase phosphorylation site:

Amino acids 63-71

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FIGURE 107

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTCACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTA
TCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCT
TTCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTCCCTGTTCTTGTA
ACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCAT
AGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTC
CTACATTAAAAATATAATGTCTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAAA
AA

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FIGURE 108

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59849
<subunit 1 of 1, 135 aa, 1 stop
<MW: 14833, pI: 9.78, NX(S/T): 0
MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL
LKALSQASTDPKESTSPEKRDMDHFFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLG
STGKSSLGTEEQRPL

Important features:**Signal peptide:**

Amino acids 1-18

Tyrosine kinase phosphorylation site:

Amino acids 36-45

N-myristoylation sites:

Amino acids 33-39;59-65

Amidation site:

Amino acids 90-94

Leucine zipper pattern:

Amino acids 43-65

Tachykinin family signature:

Amino acids 86-92

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGACGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTGTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGGAATCC
TGAGCCTTGGGTCCCCCTCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCACCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCTTCCAGTCCTGCTCTTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTGCTTGTCTGACCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

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FIGURE 111

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 112

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPR
FPWFRRNFPIPIPIESAPTTPLPSEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Homologous region to B3-hordein:

Amino acids 47-85

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FIGURE 113

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCA**ATG**GCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATAACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTGCTCTGCTCAGTGT**TAG**GTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

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FIGURE 114

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSVPPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340**N-myristoylation site.**amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292**Amidation site.**

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 115

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTATTAA
GAGATGATGGAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

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FIGURE 116

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896
<subunit 1 of 1, 166 aa, 1 stop
<MW: 19171, pI: 8.26, NX(S/T): 1
MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKK
PLMVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIM
FVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL
```

Important features:**Signal peptide:**

Amino acids 1-23

N-myristoylation site:

Amino acids 51-57

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FIGURE 117

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCGCGATCCA
GCCTAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCAAATAGACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAAATGTCAGAAAGATTGCATGGGAACT
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCCA
GTTCTCACCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTC
CCACTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGT
TCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGG
CGGCAGGCTGCCTTTTCGTTTACCAGACTCTGTTTGAACACCTGGTGTGTGCCAAGTGTGGC
AGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGT
GTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGTGCCTCAGTTCTTGGAAAGCTA
GGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCC
CCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAG
GGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACT
CATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGAC
GTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTGG
TGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAGG
GACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATCC
CCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTT
GTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGCC
CATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTAG
TTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

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FIGURE 118

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920
><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL
PPPLFSKVIVLIDALRDDVFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK
ALMTGSLPGFVDVIRNLSNPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHEVEYDGT
TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPILIGQKLSEMD
SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERK?
GDIRHPKHVQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 58-76

N-glycosylation sites:

Amino acids 56-60;194-198

N-myristoylation sites:Amino acids 6-12;52-58;100-106;125-131;233-239;270-276;
275-281;278-284**Amidation site:**

Amino acids 154-158

Cell attachment sequence:

Amino acids 205-208

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FIGURE 119

GCCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTAAGTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGG
TGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTT
GGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACC
AAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTT
ACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTGT
TTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATG
ATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTGA
ATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACCTGTAG
GGCTCATTTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCT
TCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTCA
TGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTTG
AATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAAT
ATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTTG
TGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGA
AATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGT
ACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGTG
CAATACAATAAACTCTGAAATTAAGACTC

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FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA
FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW
CKLAFYLLAFFYYLYGMIYVLVSS

Important features:**Signal peptide:**

Amino acids 1-20

Type II transmembrane domain:

Amino acids 11-31

Other transmembrane domain:

Amino acids 57-77;123-143

Glycosaminoglycan attachment site:

Amino acids 96-100

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FIGURE 121

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCCGCGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAG**ATG**GGCCCCATGGCCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCCAGTGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGAT**A**
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTCAACACATCCCCACACCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 122

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLAAKGD LVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 123

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCC
TCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCAC
AACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCA
CCCCCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCA
TGTACACACTGTGGTGGATGTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTTCGATCCGTGAGGAGAGCAGC
TACAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTA
CTCCAAGCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGT
GGACGCTGGACAAGCTCCGGCAGCGGCTCACCAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTC
AGTGGCATCCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCCCTCAAGCTGGAGCTGATCCCCGACGTGAC
CATCCCCGCCAGCATTGCCAGCTCAGGGGCTCAAGGAGCTGTGGCTTACCACACAGCGGCCAAGATTGAAG
CGCCTGCGCTGGCCTTCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCG
CTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACACCGCTA
CATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGC
CACAGGTGCTCACAGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTC
CTCAACAGCCTCAAGAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCA
CTCCATCTTCAGCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCA
TCAGCTTCAGCACCTGCACCGCTCACCTGCCTTAAGCTGTGTTACAACCACATCGCCTACATCCCCATCCAG
ATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTT
CTACTGCCGCAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTCCCTGCCGACATCGGCCTCC
TGAGAACCTCCAGAACCTAGCCATCAGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGG
AAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGCTGGGCGAGCTGACCAACCT
GACGCAGATCGAGCTGCGGGGCAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGC
GCAGCGGCTTGGTGGTGGAGGAGGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCT
GACAAGGAGCAGGCCCTGAGCGAGGCGGCCAGCAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGG
AGGGGCAGGCTAGCTTCTCCAGAACCTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGCGGGCC
GCTTGTGAGTCAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCTTTTCTCCCTCTGAGACTCACGTC
CCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTG
GAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTAT
TTTTCTCCATCTCCACCTCCTTCATCCAGATAACTTATACATTTCCCAAGAAAGTTTACGCCAGATGGAAGGTG
TTCAGGGAAAGGTGGGCTGCCTTTTCCCTTGTCTTATTTAGCGATGCCGCGGGCATTTAACACCCACCTGG
ACTTCAGCAGAGTGGTCCGGGGCGAACCGCCATGGGACGGTCAACCAGCAGTGCCGGGCTGGGCTCTGCGGTG
CGGTCCACGGCAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTT
TTAGTTTTTTGTTTTTTTTTTTTTAAATCAAAAAACAATTTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTT
GGGTATTAAGAAAGAAAAAAACTTAAAAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGG
GTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGTTGAAGTGTGTTTCCCTTCCCTGGGCGCAGGGTGAGGGTG
TCTTCCGGATCTGCTGTGACCTTGGTCCAGGAGTTCTATTTGTTCTTGGGAGGGAGGTTTTTTGTTGTTTT
TTGGGTTTTTTGGTGTCTTGTCTTCTTCTCCTCATGTGTCTTGGCAGGCACTATTTCTGTGGCTGTCCGC
CAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTCGGGTTGGCTAATCCCCGGATGAACGGTGCTCCA
TTGCGACCTCCCTCCTCGTGCTGCCCTGCCTCTCCACGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGC
CCAGACTTTGTTTTCCCACTCCTGCGGCATGGGTGTGTCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAG
CCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTAGAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGG
AGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGCTGGAGTGACACAGCCAGTCGGCACCTGGTG
GCTGGAAGCCAACTGCTTTAGATCACTCGGGTCCCACTTAGAAGGGTCCCGCCTTAGATCAATCACGTGG
ACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGTCCATCCGTCTGTCCGTCCATTTGTGTTTTCT
GCGTGTGTCTTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAATCCGTT
ACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAAATCTATAACAGAAAAA

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FIGURE 124

MRQTIKVIKFILIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLEKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLEFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKTEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 125

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCCATGAAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACCTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 126

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVR RVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLI FFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

Important features:**Signal peptide:**

amino acids 1-28

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FIGURE 127

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGGCCCGGCCTGCGCGCCCGGGCCCGCGCGCCCGCCAC
GCCCCAACCCCGGCCCGCCCCCTAGCCCCCGCCCCGGCCCGCGCCCGCGCCCGCGCCCGAGGTGAGCGCTCCG
CCCGCCCGGAGGCCCCCGCCCCGCCCCCGCCCCCGCCCCCGGCCGGCGGGGGAACCGGGCGGATTCTTCGCG
CGTCAAACCACCTGATCCCATAAAAATTATCTCTCCCGGGCGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGC
CGCCGCGCCCTCGCCCTGTGCGCCCTGCGCGCCCTGCGCACCCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGA
GCGGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCGGTAGCGGGCGGCGCCTGGATGCGGACCCG
GCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCAACCCCTACGATGAA
GAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCAT
GCCCAGGTGCGTATGCTACAATGAGCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTG
CCCGTGGGCATCCCTGCTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAG
CTTCCGTGCGTGCAGAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGCGGCTGCCT
TCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCCTGCCACA
TTCCACGGCCTGGGCCGCCTACACAGCTGCACCTGGACCGCTGCGGCCTGCAGGAGCTGGGCCCCGGGCTGTT
CCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCC
GCGACCTGGGCAACCTCACACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGT
GGGCTGCACAGCCTCGACCGTCTCTACTGCACCAAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGA
CCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCCCTGGCCCCC
TGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCCACTCTGGGCC
TGGCTGCAGAAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCGCAACGCCTGGCTGGCCGTGACCT
CAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCA
GGGCCACCGATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTG
GAGCCTGGAAGACAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGTGACAGCCCCCGGGGCAA
CGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCGCTCACTG
CAGTGCGGCCCGAGGGCTCCGAGCCACAGGGTTCCCCACCTCGGGCCCTCGCCGAGGCCAGGCTGTTACAGC
AAGAACCGCACCCGAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGG
CTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGTGTGGACAGTGCTTG
GGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCA
CGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCTGCCGCC
CGCCACCCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCAC
CCAGATCGCGGTATATAGAGATATGATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGC
TCTTTTCTTAAAAAA

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FIGURE 128

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRIFLHG NRISHVPA
ASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATFHGLGRLLHLDRCGLQELGPG
LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHG NRISVPERAFRGLHSLDRLLLHQNRVAHVH PHAF
RDLGRMLTLYLFANNLSALPTEALAPLRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVP CSLPQRLAGR
DLKRLAANDLQGC AVATGPYHPIWTGRATDEEPLGLPKCCQPD AADKASVLEPGRPASAGNALKGRVPPGDSPP
GNGSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGTGDS
EGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern:

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 129

GC GCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCCGGCACATGGCTGCAGCCAC
CTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGAGGCGCCCGGCCCGGAGGCCAA
GCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGGATGTCCCTCCTCCTTCTCCTTCTGCTAGTTTCC
TACTATGTTGGAACCTTGGGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCA
CCATCAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCCAAA
AAGTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCCTTT
GCTTCCAATTTCTGGCAGGAGATGCCCTCCTTGACAGATTGAACCTCTGAAGCCCAGTGATGAGGGCCGGTACAC
CTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCATCTTAAAAGTCTTAGTGAGACCATCCAAGC
CCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACA
GAGCCCATTGTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCCTCCCAAATCTAG
GATTGACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAGTGCA
CAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAAGTGTACAGTATGTACAAAGCATCGGCATG
GTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCCTTGGTGTGGCTGCTAATCCGAAG
GAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATTCGAGAAGATGCTGAGCTCCAAAAGCCC
GTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACA
GCAATAGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGC
ATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGCAG
AAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCTGAATTACAATGGACTTGACTCCC
ACGCTTTCCTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGAT
GAGAGGTCACTAAGTAGCAGTGAGCATTGCACGGAACAGATTGAGATGAGCATTCTTCTTATACAATACCAAA
CAAGCAAAAGGATGTAAGCTGATTTCATCTGTAAGGAGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAG
CAGGAGTCCAAATCTATTTGTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAA
AACTTTTAAATGTGGGATATTTGTATCAGTGCTTTGATTACAAATTTTCAAGAGGAAATGGGATGCTGTTTGTA
AATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTAT
TACACCTGTCTACACCATGTACTGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATT
CTGACTTAACCTTCATTTGTATAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGAGAAG
AGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACA
AAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAA
ATATATAATGGAGCAATTGTGGATTTCCCTCAAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGG
AAGGAGAAAATAACAACATGTCAATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAAT
GCTGAAAGATTACCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCA
CCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAG
AGCGGGACTCCGTCTC

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FIGURE 130

MSLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVVITYSSRHVYNN
LTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELTEGSD
LTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVR
VTVQYVQSIGMVAGAVTGIVAGALLIFLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPPSSSSSGSRS
SRSGSSSTRSTANSASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important freatures:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 131

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC
AGTCCACAGAACCCTCTCCAGGAAGCTGAATCCAGCAAGAACA**ATG**GAGGCCAGCGGA
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTCTTTCTCCTTTGGGCTTATCTCTGGCG
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTTAGGGTTG
TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAATA
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCGATCTCTG
AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTTATTCATTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATTGAACTAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACGCGCCTGAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTCAGGAG
AAAATGGGAAAATTAGTTGCTCCATTACAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCGCGCTTCACCCAAACCTCCTACACCCTGTTTCGTC
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCGAGCTCAGCGCTACAGACAGAGACTCAGG
CACCAACGCCAGGTCACCTACTCGCTGCTGCCGCCAGGACCCGACCTGCCCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGGTTCCAGTTCGCGGTGGGCGCTTCAGACCAGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGCGGTGGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGCGGGCCGAGCCGGGCTAC
CTGGTGACCAAGGTGCTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTGCGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTGGTGCCGA
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTGAAGCCGATT
ATCCCCAACTTCCCTCCCACTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
TAACCTTGGGTTCAATATTCAG**TG**ACCATAGTTGACTTTTACATTCCATAGGTATTTATTT
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
TTACTCTTGATTTTTCTCATGTTCTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

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FIGURE 132

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQVLFSLFLLGLSLAGAAEPRYSVVEETEGSSFVTNLAKDLGLEQREFSR
RQVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLLESPFEFFQAELOV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVMTSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSIADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGDGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQQAQ
ADLLTVYLVVALASVSSLFVSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSTRT
LSQSYQYEVCLAGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ
```

Important features:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 133

[illegible]

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FIGURE 134

MT PQSLLQTTLFLLSLLFLVQGAHGRGHREDFR FCSQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLQLL
SQFLKHPQKASRRPSAAPASQQLOSLESKLTSVRFMGDMVSFEEDRINATVWKLOPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTK VANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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FIGURE 135

GCCTAGCCAGGCCAAGAATGCAATTGCCCGGTGGTGGGAGCTGGGAGACCCCTGTGCTTGGACGGGACAGGGTCGG
GGGACACGCAGGATGAGCCCCGCGACCACTGGGCACATTCTTGCTGACAGTGTACAGTATTTTCTCCAAGGTACA
CTCCGATCGGAATGTATACCCATCAGCAGGTGTCTCTTTGTTTCATGTTTTGGAAAGAGAATATTTAAGGGGG
AATTTCACCTTACCCAAAACCTGGCGAGATTAGTAATGATCCCATAACATTTAATACAAATTTAATGGGTTAC
CCAGACCGACCTGGATGGCTTCGATATATCCAAAGGACACCATATAGTGATGGAGTCCTATATGGGTCCCCAAC
AGCTGAAAATGTGGGGAAGCCAACAATCATTGAGATAACTGCCTACAACAGGCGCACCTTTGAGACTGCAAGGC
ATAATTTGATAATTAATATAATGTCTGCAGAAGACTTCCCGTTGCCATATCAAGCAGAATTCCTCATTAGAAT
ATGAATGTAGAAGAAATGTTGGCCAGTGAGGTTCTTGGAGACTTTCTTGGCGCAGTGAAAAATGTGTGGCAGCC
AGAGCGCCTGAACGCCATAAACATCACATCGGCCCTAGACAGGGGTGGCAGGGTGCCACTTCCCATTAAATGACC
TGAAGGAGGGCGTTTATGTCATGGTTGGTGAGATGTCCCGTTTCTTCTTGTTTACGAGAAGTTGAAAATCCA
CAGAATCAATTGAGATGTAGTCAAGAAATGGAGCCTGTAATAACATGTGATAAAAAATTCGTACTCAATTTTA
CATTGACTGGTGCAAATTTTCATTGGTTGATAAAACAAAGCAAGTGTCACCTATCAGGAAGTGATTCTGTGGAG
AGGGGATTTTACCTGATGGTGGAGAATACAAACCCCTTCTGATTCTTTGAAAAGCAGAGACTATTACACGGAT
TTCCTAATTACACTGGCTGTGCCCTCGGCAGTGGCACTGGTCCTTTTTCTAATACTTGCTTATATCATGTGCTG
CCGACGGGAAGGCGTGGAAAAGAGAAACATGCAAACACCAGACATCCAAGTGGTCCATCACAGTGCTATTTCAGA
AATCTACCAAGGAGCTTCGAGACATGTCCAAGAATAGAGAGATAGCATGGCCCCCTGTCAACGCTTCCTGTGTTT
CACCTGTGACTGGGGAATCATACCTCCTTTACACACAGACAACATATGATAGCACAAACATGCCATTGATGCA
AACGCAGCAGAACTTGCCACATCAGACTCAGATTCCCCAACAGCAGACTACAGGTAAATGGTATCCCTTGAAGAA
AGAAACTGACTGAAGCAATGAATTTATAATCAGACAATATAGCAGTTACATCACATTTCTTTCTCTTCCAAT
AATGCATGAGCTTTTCTGGCATATGTTATGCATGTTGGCAGTATTAAGTGATACCAAATAATACAACATAACT
TTCATTTTACTAATGTATTTTTTGTACTTAAAGCATTTTTGACAATTTGTAAAACATTGATGACTTTATATTT
GTTACAATAAAAGTTGATCTTTAAATAAATATTATTAATGAAGCCTAAAAAAAAA

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FIGURE 136

MLPRWWELGDPCAWTGQGRGTRRMSPATTGTFLLTVYSIFS KVHSDRNVYPSAGVLFVHVLEREYFKGEFPPY
PKPGEISNDPITFNTNLMGYPDPRPGWLR YIQRTPYSDGVLYGSPTAENVGKPTIIETAYNRRTFETARHNLI
NIMSAEDFPLPYQAEFFIKNMNVEEMLASEVLGDFLGAVKNVWQPERLNAINITSALDRGGRVPLPINDLKEGV
YVMVGADVFPSSCLREVENPQNQLRCSQEMEPVITCDKKFRTQFYIDWCKISLVDKTKQVSTYQEVIRGEGILP
DGGEYKPPSDSLKSRDYYTDFLITLAVPSAVALVFLILAYIMCCRREGVEKRNMQTPDIQLVHHS AIQKSTKE
LRDMSKNREIAWPLSTLPV FHPVTGEIIPPLHTDNYDSTNMPLMQTQQNLPHQTQIPQQQTGKWYP

signal sequence:

Amino acids 1-46

transmembrane domain:

Amino acids 319-338

N-glycosylation site:

Amino acids 200-204

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 23-27

Tyrosine kinase phosphorylation site:

Amino acids 43-52

N-myristoylation sites:

Amino acids 17-23;112-118;116-122;

185-191

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FIGURE 137

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT
GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCA**ATGG**GCTCCGCAGAACCTGAGCACCTTTT
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGGTGCCCTCGAAGTGCCTCTATAAAGGATATTAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGAG**AGTG
AATAAAATTGGACTTTGTTTAAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGGAAGAATGACC
AGCAAAAGGTTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
TTATTTT

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FIGURE 138

MAPQNLSTFCILLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHFDNRNPDDPQAQEKFDLGAAY
EVLSDSEKRRKQYDTYGEGLKDGHQSSHGDI FS HFFGDFGFMFGGT PRQQDRNIPRGSDIIVDLEVTLEEVYAG
NFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCECPNVKLVNEERTLEVEIEPGVRDGM EY
PFIGE GEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDG HKVHISRDKITRPG
AKLWKKGEGLPNFDN NNIKGS LIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 139

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCTGTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 140

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVDGIGQTLVPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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FIGURE 141

GGCGCCGCGTAGGCCCCGGGAGGCCGGGGCCGGCCGGGGCTGCGAGCGCCTGCCCCATGCGCCCGC
CGCCTCTCCGCACG**ATG**TCCCCCTCGCGGAGGAAAGCGGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT
GCCCTTCCGCGAAGCCTTCGAGGAGCTCCTGGTCTTTCGTGCCCCACATGCGCCGCTTCTCTGA
GCAGGAAGAAGATCCGGCACCAATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTTCTTGAGGCTGGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTTCGGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCCTCGGGAATCACAACCTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGGCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTGCTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCTGCCTTCTGCTCACCCCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCC
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL SLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 143

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGGCAGATGTTGGGG
CTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAA
AAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTGCTCTCTTCTTACTGGTTTTGCACC
ATAACTTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATA
GACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGGTGCATCGCTGCATC
TGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAATGTGATTTTCT
ACATTGTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCCTAACTTTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCAT
GAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATG
ATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTT
TCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTA
TCTTGACTATAAAAAAGGAAAAGAATTCGTAAGCTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTT
TTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTAACCCTGGAATAATGGATGAACTCAATGTA
GAAGAGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACA
GCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGT
TTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGAT
GTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCACCTAATCOGAAGATATACCGAGATCTCAA
CATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGCTAGCTAGGTAAAGATGACA
AACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGT
GTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAT
TCAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAACTTACATTTTTC

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FIGURE 144

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDR LGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWIIPDPTGKFNLIRRYTEISNIK

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FIGURE 145

AAACTTGACGCC**ATG**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAG**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

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FIGURE 146

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLGKLSATPDAQ

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FIGURE 147

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

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FIGURE 148

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGKPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 149

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTT CAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA
GTT CATGCAAAATGAGTGTGTTT TAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 150

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHERPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 151

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 152

MSRSSKVLGLSVLLTAATVAGVHVKQQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

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FIGURE 153

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGC**ATGGA**ATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTGATCACTT
ATATCTGGAACCAAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTTCATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTCCTCGGTGGGAGGCCACCCCATGGACCGCTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCG**TAA**AGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAAA

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FIGURE 154

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPV
SNDPDNPCSLKCQAKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLG
STVKEDNCGVCNGDGSTCRLVRGQYKSQLSATKSDDTVVALPYGSRHIRLV
LKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNSSVDFQKFDPKEIL
RMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFEPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP
CPASDGYKQIMPYDLYHPLPRWEATPWTACSSSSCGGGIQSRAVSCVEE
DIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWLAQEWSPCTVTGQGL
RVRVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKL PVEAKLPWFKQAQEELEGA AVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 155

[illegible]

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FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSGQGLGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGGQGNNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSSGGSSSSGGSSSSGGSSSGSGSSGSGSSGSGSSGSGSSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:
amino acids 1-21

N-glycosylation site.
amino acids 265-269

Glycosaminoglycan attachment site.
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.
amino acids 301-304

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FIGURE 157

[illegible]

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FIGURE 158

MDFLLLGCLCYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHNLSGLLGLSLRY
NSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQITQLPNTTFRMPNLRSDLSYNK
LQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDIV
KVNFAHFPRLLISLHSLCLRRNKVAIVVSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIE
PRIILNSWKSLSITLAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAET
SGHLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLIVVL
VLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVIINEYGSCTCHQQPAR
ECEV

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FIGURE 159

CAGAGAGGAGGCTTTGGGAATTGTCCAGCAGAAACAGAGAAGTCTGAGGTGGTGTCAAGACA
AAAGATGCTTCAGCTTTGGAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT
CTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCTGTTCTTCA
CGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTGACCC
TAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCAGGAAGCTGAG
AAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACCTAACACGGACATTTTTGGGTTGAA
AATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTA
ACCTGAGCTTCCCTGTCACCCGCGAATGTCACTGTGGCCGGGCCCATCATTTGGCCAGATTATC
AACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTGACCAATTGAAACTGATCCCCAGACACA
CCAGCCTGTTGCCGTCTTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCTTGC
TGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGC
ACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCT
GGATGTGAATGTCATTGAGCAGGTGCTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCC
TCATCTGAAGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCAGTGGCT
TGCCCCACCCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAA
AGCCTGAGTCCCACCAGAAGGACCTTCCCAGATACCCCTTCTCCTCACAGTCAGAACAGCAG
CCTCTACACATGTTGTCCTGCCCTGGCAATAAAGGCCCATTTCTGCACCCTTAA

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FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59622
><subunit 1 of 1, 249 aa, 1 stop
><MW: 27011, pI: 5.48, NX(S/T): 2
MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKV
DLGVLQKSSAWQLAKQKAQEAELNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDG
KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECDPTS
ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ
HKTQLQTLI
```

Important features:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 124-128;132-136

N-myristoylation sites:

Amino acids 12-18;16-22;26-32;101-107;122-128;141-147

Leucine zipper pattern:

Amino acids 44-66

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FIGURE 161

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTATCGGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT
GAGCATTCAAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCCTTCA

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FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLM
LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW
APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCM
PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV
GQVCQETLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCN
SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG
GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGV
GLALAPALWWGVVCPSC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domain:

Amino acids 243-260

N-glycosylation sites:

Amino acids 46-50;189-193;382-386

Glycosaminoglycan attachment sites:

Amino acids 51-55;359-363

N-myristoylation sites:

Amino acids 54-60;75-81;141-147;154-160;168-174;169-175;
198-204;254-260;261-267;269-275;284-290;333-339
347-353;360-366;361-367;388-394;408-414;419-425

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FIGURE 163

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTGAGAAGAGCCAC
AGCATAAGAGACTGCCCTGCTTGGTGTTCAGGATGATGGTGGCCCTTCGAGGAGCTTCTGCATTGCTGGTT
CTGTTCTCTGCAGCTTTTCTGCCCCGCGCAGTGTACCCAGGACCCAGCCATGGTGCATTACATCTACCAGCG
CTTTCGAGTCTTGGAGCAAGGGCTGGAAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCGAAGAGT
TCTCAAAAAATATATCTGTCTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAAC
TTGGCACTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTGACGAGTGCAT
CGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAAGATCCGGACTCTGC
TGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAATAGTGAAGAAGATGATGGACACACAT
GGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAAGGTGTAATTAATTGGATCCAGAAACAACACTGT
TTGGGAATTTGCAAACATACGGGCATTCTGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACAC
TTTCCTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTCTATAACCAAGCAACTTCTAATGAG
ATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCAGGAGGGGTAGGCCGAGCATT
GGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCTCTGGGCCATCCACTCTG
GGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCTAGGGAT
ACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGG
GGGCCAGGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACT
TGTTCTTCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCCTGG
AATGAAGGAAACCAGATCATTTCACAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAAATGCATTACAGCTGT
GAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGCCCCCTTCACAAATATAGTATCC
CTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAAATACGSTATGCCTCCTTTCCCAAATGTCACTGCCTTAG
GTATCTTCCAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAACCTC
CTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACTGCTCCCGAGCATTTC
TGTAACCTTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCTAATATTACCACTGGCTTTTCTCT
CCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTCAAATGTCTATTGATATTCTCCCAATTTCACTGCCCAACT
AAAATACTATTAATATTTCTTCTTTTCTTTTCTTTTGTGAGACAAGGTCTCACTATGTTGCCAGGCTGGT
CTCAAACCTCAGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCACCA
CACCTGGCTTAAATACTATTTCTTATTGAGGTTAACCTCTATTTCCCCTAGCCCTGTCTTCCACTAAGCTT
GGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTCCAGGTGTGGAGTGTTCACATCAT
TGAATTCTCGTTTACCTTTGTGAACATGCACAAGTCTTTACAGCTGTCACTCTAGAGTTTAGGTGAGTAACA
CAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTCATTGCCCCAAGGAAGCATCA
AATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC
TTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTC
TAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTCTGTTTCTCTTTCTGCTTTAAATTCA
ATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

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FIGURE 164

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEFKSNISVMLGRC
QTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLLQEAEKKIRTLLNASCDNMLMGI
KSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTVWEFANIRAFMEDNTKPPAPRKQILTLWQGTGQVIYK
GFLFFHNQATSNEI IKYNLQKRTVEDRMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLT
IEPGTLGVEHSWDTPCRSQDAEASFLLCGVLYVVYSTGGQGPHERITCIYDPLGTISEEDLPNLFPPKRPRSHM
IHYNPRDKQLYAWNENQIIYKLQTKRKLPLK

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FIGURE 165

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGCAGTGTTTTGCC
TTCACCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCCTCCTAGTAACTGTGTCTGACTGTG
CTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGTGGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTT
CGAGGGCTGCGGATGTGCACCCCGCTGGGGCGGGAAGGCGAGGAGTGCCACCCGGCAGCCACAAGGTCCCCTT
CTTCAGGAAACGCAAGCACACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGACGGCAGGT
ACCGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCACCATCCTTTT
CCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCAGTCCCTACACTGACT
ACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATACCTCCCATCATGACATGGTCCCCAG
GCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGC
TGCCAGAGAGGTGGTAAATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCCCTGGGC
CCTGCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGTGCATTGCT
CAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTGTGGGTAGTTCA
TCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTTCCCAGAGGGCAGCAGAC
AGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCT
GTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTT
ACCAGTTAACCCTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAATCTAAT
CTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCAAGGATCAGCCCTGAGAGC
AGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGCAGGGCAGGG
GCTGAAAGGGGCACTGATTGAGACCAGGGAGGCACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAA
CTGAAAAAA

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FIGURE 166

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHPGSHKVPFFRKRK
HHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Important feratures:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 167

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGGTGTGGAGCCC
TCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTATGGCAAGAGCTCTACTCGTGCGG
TGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTG
CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAAATGCACTTTCTCCAGCTTTGCCCCGTGGGTGATGCTCT
AACAGTGACCTGGAATTTTCGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCT
TCCAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCCATC
CTTCTCTGGAACTGCAGTTCGACGACAATGGGACATAACCTGCCAGGTGAAGAACCCACCTGATGTTGATGG
GGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCA
TTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGA
TGGGCCGAAAGAGCTCATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGT
CTCTGTTTATTTAGAAGACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTA
GTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTCCAACCAGTTCTGCAGC
ATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATATCACCAGTCATACACAGC
CTCATTATTAAGGTCTTATTTAATTTTCAAGTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAG
CTACATTTTTGCCCTTAAGACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGGATA
AAAGCCAATTTGTCTGTTACATTTCTTTTACGATTTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGT
TTACTCTCTTTCTTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAAACAGTAAA
TCCTAAATTCAAACCTGTTAAATGACATTTTATTTTTATGTCTCTCCTTAACTATGAGACACATCTGTTTTAC
TGAATTTCTTCAATATTCAGGTGATAGATTTTGTCTG

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FIGURE 168

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTWNFRPLDGGPEQ
FVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVKNPPDVDGVIGEIRLSVVHTVRF
SEIHFLALAIGSACALMIIIVIVVVLFFQHYRKKRWAERAHKVVEIKSKEERLNQEKKVSVYLEDTD

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FIGURE 169

GAGCGAAC**ATG**CCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTAATCCGTTATCGTCATGTTCACTGCT
CTCCAAGTGCATAGACAGTGTGTCGTTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGCCATGGTGGATTTTG
ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
CCTGCAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTTGGCTGTTATTGGTGGACTTGTGTAT
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTG
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGGCTTTTATG
TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTTCTGATGAGT**TAAAA**AGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAGAAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
CCCAGTGAAGTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTGGTCACTCTGAT
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
ACTTTACGCATCTTTCCCTTTTGAGTAGAGAAATTATGTGTGTGATGTGGTCTTCTGAAAATG
GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAATA
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTTGAAGTCAAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 170

MAARWRFWCVSVTMVVALIVCDVPSASAQRKKEMVLSEKVSQLMWETNKRVPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

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FIGURE 171

CTCCACTGCAACCACCCAGAGCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTTTCTGCATCTCC
AGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGATGCTGTGCCAGCCACACAAGAG
ATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTTGCTATGATGATGCCGTCGTGCCCTTGCCAGGACCC
AGACGTGTGGAACTGCACCTTCAGAGTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATA
AACCAGAACTGCGACTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTTAATGGAACATCAGGGG
AACGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGATGC
TGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATTCTGTGACCTGTCTGAGGGCCAC
CCTGCAGCTGCCCTGAGGAGGCCCCACAGTCCCCTTCTAGAATTCTGGACAGCATGAGATGCGTGTGCTGATGG
GGGCCCAGGACTCTGAACCTCCTGATGACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTG
GGGAACCTTCACCTTCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATC
ATAATAAATTTATGTACTTTATAAATGAAAA

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FIGURE 172

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPLARTQTCGNCTF
RVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 173

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCCTCT
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC
CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGGCAGAACGTCACCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACCGCCGTGCCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAAACC
CCGGCTTTGAAGCCTCACCACTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCCCTG
TCCTATGTGGCCACGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCCTGTCCCTGACT
CTCCAAACTTTGAGGTCACTTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCCTGTTCCAAGGATTTTGGGGTGCTGAG
ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTGGCCGAGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTCRLLGPVVK
GHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENIATAALATGACIVGILCLPLILLVYKQRQAASNRRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 175

[illegible]

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FIGURE 176

MDSLRLKMLISVAMLGAGAGVCYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLATLQEAATTQENV
AWRKNWMVGGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 177

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCGTGCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCC**ATG**AGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCCGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCCCTCCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA
CTCG**TGAC**TGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG

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FIGURE 178

MRGSQEVLLMWLLVLAVGGTEHAYRPGRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

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FIGURE 179

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
CTCTCATGCTCAGTTTGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAAGTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCCTCTCATTTCCATCACGGGATATGTT
GATAGAGACATCCAGCTACTCTGTCTGTCAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAAGTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGAATATGAGTG
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAAGTCCC
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG
GTGAAAT**GTAG**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

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FIGURE 180

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELOWRRKHGQAELOWRKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

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FIGURE 181

GC GATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCAACGAGGAGAAGA
TGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGG
CGGCCTCGCCCTGTTGTGCTGCGCCGCGCCGCGCCGCGCCGCTCGCCTCAGCCGCTCGGCGGGGAATGTCACCG
GTGGCGGCGGGGCGCGGGGCAGGTGGACGCTGCGCGGGCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTC
CCTAGGGCGACGGCTCCACGGCCCGAGGCCCGAGGACCGGGCCCCGCGCGCCACCGTCCACCGACCCCTGGC
TGCGACTTCTCCAGCCAGTCCCGGAGACCCCTCTTTGGGCGACTGCTGGACCTCTTCCACCACCTTTC
AGGCGCCGCTCGGCCCTCGCCGACACCCCTCCGGCGGGGAACGCACTTCGACCACCTCTCAGGCGCCGACC
AGACCGCGCCGACCACCCCTTCGACGACCACTGGCCCGCGCGGACCACCCCTGTAGCGACACCGTACCGGC
GCCCACGACTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAACAGCAGCGTCTCCCCACCCACCTG
CCACCGAGGCCCCCTCTCGCCTCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAAT
CGCTGCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTATCAGGGGCTTCACTGTGAAACCTGCAAAGA
GGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCATGTGACTGTAGTCCACATGGAGCTCTCAGCATAC
CGTGCAACAGGTAAGCAACAGAGGGTGGAACTGAAGTTATTTTATTTTAGCAAGGGAAGGCTGCTA
CTCTCAAGGACCATACTGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTA
TTCTCTTACTTTATATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAG
CACTAGAGTCGCAATTTTCTCTGGGATAATTTCTGTAAATTTATGGGAAAAATATTGAAGAATAAATCT
GCTTTCTGGAAGGGCTTTTCAAGCATGAAACCTGCTAGGAGGTTTGAAGATGTTCTTATGTTTATTAATATACCA
TTGGAGTTTGAGGAAATTTGTTGTTGGTTTATTTTCTCTCTAATCAAAATTTCTACATTTGTTTCTTTGGACA
TCTAAAGCTTAACCTGGGGGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAG
TACATTTTGGAGACCAAAGTAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAAT
CTAGTGAATAATGTACTGTTATCTAAGCATTGCTTGTACTGCACTGAAAGTAATATTCTTTGACCTTATG
TGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATG
ACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGCCACTTACGAGCTGTGTTCTTGGGCAAG
TAATTTCTTTTCACTGAGCTTGTTCCTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGC
CTAGCACATGTCACTCAATAAATTTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACA
TGTTTTAAGAACTTTTAGCTCCTTGACAAAGAAGTGCTTTTAACTTTAGCACTAAATATTTTAAATGCTTTATA
AATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTTAAATGTTAGAGGCTGGGCGCGGT
GGCTCACGCTGTAACTCTAGCACTTTGGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGA
GCCTGGCCAGCACAGTGAAACCCGCTCTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCT
GTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGA
GATCGCGCCACTGCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRELAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTTLSTTTGPAPTTFPVATTVPAPTTTPRTPTPDL PSSSNSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 183

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGTCTCGGTGCCCCA
GGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCCTGAGCAGCTTCTTGGGCCCTGGTACGTGCTTGCGGTGGCC
TCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGA
AAACAACCTGCGGACGCTGTCCTCTCAGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGC
GAAACTCCGGATGGGTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGA
GACTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCTGAC
GGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTTCCTGTCACAG**TAGC**
AGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGG
CGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCT
CAGAATAAAGCGATTCCACAGCA

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FIGURE 184

MGGLLLAAFLALVSVPRQAQVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVTLTPENNLRTLSS
QHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQLEFGDEPFNTVELYSLTETASQEAM
GLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20

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FIGURE 185

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCCGGGACTGGAAGTCATCGGGCAGAGGTCTCACAGCAGCCAAGGA
ACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATCCTGCTTGCTCTGGCAACAGGGC
TTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAGTGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTG
TTCGAGAAGACGCGGCTACTCTGTGGGGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCT
CAAGCCCCGCTACATAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAG
CCACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGCTG
GTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCACGCTGTGTCACTGC
TGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAGTTACGCTGCCTCACACCTTGCGAT
GCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTG
TGTGCCAGCGTGCAGGAAGGGGGCAAGGACTCCTGCCAGGGTGAATCCGGGGGGCCCTCTGGTCTGTAACCAGTC
TCTTCAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCT
GCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCATCACCC
TCCATTTCCACTTGGTGTTGGTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCCAAGACCTCTACGAACA
TTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCT
GGATTCAAATTCTGCCTTGAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCA
GCCCCAAAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 186

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQ
HNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITWAVRPLTLSSRCVTAGTSC LISGWG
STSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCASVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQD
PCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 187

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG
ACCATGGTGCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCCTTTATACC
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
CTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
GAGAATCTCAAAGTCTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT
GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
CAGCTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAAC
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGAT
TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT
CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
GCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
TTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCCAGTGATCGTGTGTCGCTGCAAC
GTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC
AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCTCATTTTACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
ACTGTCTTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
TTTATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTTTGCCCAATAATAAAGCCCCA
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 188

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAQYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPRLAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDE
GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPPKLDQESYEASVPISAPAGSFLLTIQSPDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHII PVVVSHNAQMWQLLV RVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 189

[illegible]

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FIGURE 190

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRLTRIPSNLSSDT
QVLLQLQSNNIAKTVDELQQLFNLTELDIFSQNNFTNIKEVGLANLTQLTTLHLEENQITEMTDYCLQDLSNLQEL
YINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVGILDMNFKPLANLRSVL
AGMYLTDIPGNALVGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINN
MGELVSVDRYALDNLPELTKLEATNNPKLSYIHRLAFRSVPALESIMLNNNALNAIYQKTVESLPNLREISHS
NPLRCD CVIHWINSNKTNI RFMEPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGTTVF
LDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNVQGADTRVATIKVNG
TLLDGTQVLKIYVKQTESH SILVSWKVNSNVMTSNLKWSSATMKIDNPHITYTARVPVDVHEYNLTHLQPSTDY
EVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETSTALAAVMGSMFAVISLASIAVYFAKRFRKKNYHHSLK
KYMQKTSSIPLNELYPPLINLWEGDSEKDKDGSADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

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FIGURE 191

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGC
TGCAGAAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTTAAACTGGCATCCGGCCTTGTCTGGGAGAATAATGTGCGCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTGTGAATAAACTTGATACACCA

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FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1; 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFENGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNVQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 193

GAAGTAGAGGTGTTGTGCTGAGCGGCGCTCGGCGAACTGTGTGGACCGTCTGCTGGGACTCC
GGCCCTGCGTCCGCTCAGCCCCGTGGCCCCGCGCACCTACTGCCATGGAGACGCGGCCTCGT
CTCGGGGCCACCTGTTTGTGCTGGGCTTCAGTTTCCTGCTCCTCGTCATCTCTTCTGATGGACA
TAATGGGCTTGGAAAGGGTTTTGGAGATCATATTCATTGGAGGACACTGGAAGATGGGAAGA
AAGAAGCAGCTGCCAGTGGACTGCCCCTGATGGTGATTATTCATAAATCCTGGTGTGGAGCT
TGCAAAGCTCTAAAGCCCAAATTTGCAGAATCTACGGAATTTTCAGAACTCTCCCATAATTT
TGTTATGGTAAATCTTGAGGATGAAGAGGAACCCAAAGATGAAGATTTTCAGCCCTGACGGGG
GTTATATTCCACGAATCCTTTTTCTGGATCCCAGTGGCAAGGTGCATCCTGAAATCATCAAT
GAGAATGGAAACCCAGCTACAAGTATTTTTATGTCAGTGCCGAGCAAGTTGTTTCAGGGGAT
GAAGGAAGCTCAGGAAAGGCTGACGGGTGATGCCTTCAGAAAGAAACATCTTGAAGATGAAT
TGTAACATGAATGTGCCCTTCTTTCATCAGAGTTAGTGTTCTGGAAGGAAAGCAGCAGGGA
AGGGAATATTGAGGAATCATCTAGAACAATTAAGCCGACCAGGAAACCTCATTCCTACCTAC
ACTGGAAGGAGCGCTCTCACTGTGGAAGAGTTCTGCTAACAGAAGCTGGTCTGCATGTTTGT
GGATCCAGCGGAGAGTGGCAGACTTTCTTCTCCTTTTCCCTCTCACCTAAATGTCAACTGT
CATTGAATGTAAAGAATGAAACCTTCTGACACAAA

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FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67300
><subunit 1 of 1, 172 aa, 1 stop
><MW: 19206, pI: 5.36, NX(S/T): 1
METRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHWRTLEDGKKEAAASGLPLMVI
IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEPEKDEDFSPDGGYIPRILFLDP
SGKVHPEIINENGNPYKYFYVSAEQVVQGMKEAQERLTGDAFRKKHLEDEL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Thioredoxin family proteins:

Amino acids 58-75

N-myristoylation sites:

Amino acids 29-35;67-73;150-156

Amidation site:

Amino acid 45-49

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FIGURE 195

CGGCTCGAGTGCAGCTGTGGGGAGATTTCACTGCATTGCCTCCCCTGGGTGCTCTTCATCTTGGATTGAAAGT
TGAGAGCAGCATGTTTTGCCCACTGAACTCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCCTGAATG
ACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTGGGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGC
ACAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCT
ATACTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCTGACACTTATGGGGGACATCTTAT
GCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCCTC
AAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGT
CCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAAT
GGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTATTTGTTACTACCACAACTCAGGATGTCTGTGGAG
TACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCAT
CATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGGAACCTGGTGTCA
AGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTG
GTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGAT
ATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCACTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGA
CTAATCCAGAGATAAAGAAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATA
ATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGT
TTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAACACAGC
AAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGC
CACTCTACCAAGTATTTTCACTCTCCGCTCTCCAGCTGTCCTCCTGTCTCATTGTTTGGTCAATACACTGAAG
ATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATG
GACTTGGCCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGAT
CAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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FIGURE 196

MFCPLKLILLPVLLDYSIGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTLSPGEHAKDEYVLYYY
SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGT YICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVG
GLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL RMSVEYSQSWG HFQNRVNLVGDI FRNDGSIMLQ
GVRES DGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIV
KKT CGNKSSVNSTVLVKN TKTNPEIKEKPC HFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPS
LRSDRNNSLEKKSGGMPKTQQAF

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FIGURE 197

CGCCATGCCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTTCGACG
CTGTTGGCGCTGCTCGTGTGCCCCGCGCGGGGTTCGCGGCGGCGGGGACCACGGGGACTGGGA
CGAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCG
TGACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGC
CGGCCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCC
CTATTTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTA
CACTGACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGT
CCCCTTTGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGA
TATTGCAAAGCATTTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATA
ATTGGTTCTTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCA
AAAATCGTGACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAAT
TTAGCAACACTTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAAGGCTTAATGTTTCT
CTGGAAAGCGTCCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 198

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPOSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ

Important features of the protein:**Transmembrane domain:**

Amino acids

11-29

N-glycosylation sites:

Amino acids

160-164;193-197;216-220

N-myristoylation sites:

Amino acids

3-9;7-13;69-75;97-103

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FIGURE 199

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTCCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCTACCTCTGGGA
TTGTCTTTGTCTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCC
GCCATCTCTCGGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGACTGAGGATATTTAAAATTCATTT
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCAAGAGTTCCCTGCTGCTGCTGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCCACCTCCGGAATTCTGACCTCTGTTTCCCTCCGTCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

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FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGP SHYMARYSTSAPAI SRGPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 201

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTCTCCTTCTGCTC
TGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAAAAAAGTGGACTGCAGCATTTA
CAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACATACCTACCAGTTTGTGGTTCTGACTACATCACCT
ATGGGAATGAATGTCACCTTGTGTACCGAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGT
TGCTTAAATTCTCCATGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGAC
TGAGTTTCTTTAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTGAGAGTAATCTTGACTGAATGGA
GAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTTAACACGTCAATAA
AAAAATAATCTCCAGA

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FIGURE 202

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNECHLCTESLKSN
GRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 203

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGGCCCTGGCTGCGGCGCTG
CTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCTCGTCGCTCAGCCCCCTATTTCCG
CACCAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGTGCGGGCCCGAGGCTCCGTGGCGGGACCCCTGAGC
TGCTGGAGGGGACCTGCACCCCGGTGCAGCTGGTCGCCCTCATTGCGCCACGGCACCCGCTACCCACGGTCAAA
CAGATCCGCAAGCTGAGGCAGCTGCACGGGTTGTGTCAGGCCCCGCGGTCCAGGGATGGCGGGGCTAGTAGTAC
CGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGCTAG
TAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGGCCCTTTTCAGCCGT
GAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCCTGCGATGGATAGCAGCGCCGCTTCCCTGCA
GGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCGCCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAG
TTAATGATAAACTAATGAGATTTTTTGTACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCT
CTTTATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTAAAAAAGTTGCAGCTACTTTGCA
AGTGCCAGTAAATGATTTAAATGCAGATTTAATCAAGTAGCCTTTTTCACCTGTTTCATTGACCTEGCAATTA
AAGGTGTTAAATCTCCTTGGTGTGATGTTTTGACATAGATGATGCAAGGTATTAGAATATTTAAATGATCTG
AAACAATATTGGAAAAGAGGATATGGGTATACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTT
TCAGCACTTGGACAAAGCAGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTG
GTCATGCAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTAC
AATTACAAAAACAAATGCATCGGAAGTCCGAAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGT
GCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAAATCCGAGTGCAGATGTTATTAATGAAAAGGTGT
TACCTTTGGCTTACTCACAGAACTGTTTCATTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAG
AGTTGTCAAACCAAGTGAAGAATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAAGTGAAGTGAAGA
ACATTTTAAATCTTTAGGAATCTGCAATGAGTGATTACATGCTTGAATAGGTAGGCAATTCCTTGATTACAG
GAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATG
AAATGTAAGAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGCC
CTGCAATGTTTACAGAAATGAAATCTTCTACTTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTT
ATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCATCCTTAAGTTGATTGAAGTGTCTA
GGAACCTTACAGATTGTTCTGCAGTTCTCTCTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATCAG
GAATATTGTGTTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAAC
AGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAAATATTTTGGTATTTAT
TTATGAAATATTTGAACATTTTTTCAATAATTCCTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTA
TTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACT
TTTTTCATTCTGTCACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTGTGTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAATAAGAAAATTC
TTGTGACTTTAAAAAAA

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FIGURE 204

MLRAPGCLLRTSVAPAAALAAALLSSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLSGPEAPWRDPELL
EGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRDLGAALADWPLWYADWMDGQLVE
KGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMDSSAAFLOGLWQHYPGLPPPDVADMEFGPPTVN
DKLMRFFDHCEKFLTEVEKNATALYHVEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKG
VKSPWCDVFDIDDAKVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGH
AETLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEKVLP
LAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSEDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 205

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGT**AGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW**Signal peptide:**

amino acids 1-20

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FIGURE 207

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

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FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

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FIGURE 209

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCT
GCCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTCTGTGCGAGGCCGAGGT
GGGCGTGAAGGGCACAGACCGCCTTGTAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCCTG
ACCGGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGC
CTACAAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGA
GGACTGCCGTGCTCAACGTCTATAGCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCAATGGTATGGG
TCCATGGAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCATGGGGATGTG
GTCGTGGTTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAAGCACTGGAGATGAGCATGCACCTGGCAA
CCAGGGCTTCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCA
ACTGTGTCACTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCA
GGGCTGTTCCACAGAGCCATCACACAGAGTGGGGTCAACACCCAGGGATCATCGACTCTCACCTTGGCC
CCTAGCTCAGAAAATCGCAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGC
AGAAAGAAGGAGAAGAGCTGGTCCCTTAGCAAGAAGCTGAAAATACTATCTATCCTCTCACCGTTCATGGCACT
GTCTTCCCCAAAAGCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAA
CAACCATGAGTTCAGCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATACAATGGAGCAGATGAGCCGGGAGG
ACATGCTGGCCATCTCAACACCCGTCTTGACCACTCTGGATGTGCCCTTGGAGATGATGCCACCGTCAATAGAT
GAATACCTAGGAAGCAACTCGGACGCACAAGCCAATGCCAGGCGTTCAGGAATTTCATGGGTGACGTATTTCAT
CAATGTTCCACCGTCAGTTTTTCAAGATACCTTCGAGATCTGGAAGCCCTGTCTTTTCTATGAGTTCAGC
ATCGACCCAGTCTTTTGGCAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTG
TTCGGAGGTCCCTTCTCATGGACGAGAGCTCCCGCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCT
AAGCCTCACCATGATGGCCAGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTT
GGCCCCAATTCAACCAGGCGGAACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTCAGGGAG
GCCTGGATGCAGTCTGGTCAGAGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAA
GGCCAGGAGGACCTCTGAGGCCAGGCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAG
TCCCAGCACGGCAGCCCGCTCTCCCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCT
GTGACTGGAGTTATGCTCTTTTGAATGTCAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTCTTCCC
TCTCCCTGAAGTGCCCTTCTGCTTTCTTCTGTTAGTCTTAGCACATTCTCTAGCTTCTGGAGGACTCAC
TCCCCAGGAAGCCTTCCCTGCCTTCTCTGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCC
GAGGCTAGCACCGTGTCTGTGTCTGTCTCCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCAC
TCTGTCAACCCACACCAGGATCGGGTGGGACCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAACACAGA
ATATGGGAATGGCAGCTGCTGAACCTGAACCCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGAC
ATTGTCCACCCTGGCCAGAAGGGTGATGCCAATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGG
GATCCAGCCTAGAGCAGACCTTAGCCCCCTGACTAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTGTC
TGCCAGTCTTGGCCCCCTGCACAAGACAACAGAATCCATCAGGGCCATGAGTGTACCCAGACCTGACCTCAC
CAATTCCAGCCCTGACCCTCAGGACGCTGGATGCCAGCTCCAGCCCCAGTGCCGGGTCTCCCTCCTTCTCT
GGCTTGGGGAGACCACTTCTGGGGAGCTTCCAAGAGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGG
CATCTGGACAGGGCATCCGTGCGGCTATTGTACAGAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGG
TGAAAAGCACCAAGAGGTTTTAGATGGAAGTGAGAGGTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTG
CTCTCCCTGCCGCTCTGCTGGGCTCCCACTTTGGCAGCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGT
AGGAGCCCTTCTGGGCTGGCCAGGCCGAGCCAGCTCCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGG
CGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGCCAGAGTGAAGTCCGGGTGGGCGTGGGCTCGGCGGGG
CCCACTCAGAGCAGCTGGCCGGCCCCAGGCACTGAGGGCCTTAGCACCTGGGCCAGCAGCTGCTGTGCTCGATT
TCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGGGACCTGCAGCCCTCCATGCCTGACCTCCCC
CACCCCCCTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAGCGCCGCCCTCTGCTCCACAGCGCCAGTCCC
ATCGACACCCCAAGGGCTGAGGAGTGCAGGCTGCACAGCGCGGCACTGGCAGGCAGCTCCACCTGCTGCCCACT
GCTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGGGACTTGGAGAACCTTTATGTCTAGCTAA
GGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCTGTGT
CTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCTACTCTGGTGGGGACTTGGAGAACCTTT
GTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCTTTGTGTCTAGCTCAGGGATCGTAAAC
GCACCAATCAGCACCTGTCAAAACAGACCACTTGACTCTCTGTAAATGGACCAATCAGCAGGATGTGGGTGG
GGCAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCCCCCTCGGGTCCCTCCACGCGCT
GGAAGCTTTGTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

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FIGURE 210

MERAVRVESGVLGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGKGTDRLVNVFLGIPFAQPPLGPDR
FSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLVLVNVYSPAEPVAGSGRPVMVWVH
GGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFFSTGDEHAPGNQGFDDVVAALRWVQENIAPFGGDLNC
VTVFEGGSAGGSIISGLVLSFVAAGLFHRAITQSGVITTPGIIDSHPWPLAQKIANLTLACSSSSPAEMVQCLQQK
EGEELVLSKKLKNTIYPLTVDGTVPKSPKELLKEKPFHSPVFLMGVNNHEFSWLIIPRGWGLLDTMEQMSREDM
LAISTPVLTSLDVPEMMPTVIDEYLGNSDAQAKQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEFOHR
PSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMMAQWTHFARTGDPNSKALPPWP
QFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKAQEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161, 162-168, 217-223,
227-233, 228-234, 232-238, 262-268, 357-363, 461-467**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 211

AACTTCTAC**AT**GGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACAC
CATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCC
GGGAGCACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTG
GTTTCATGCCAGCCTGTAAAAGGCCATGGAACTTTGGGTGAATCACCGATGCCATTTAAGAG
GGTTTTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTAGTAGCC
ACCAGCCACCTGTGGCCGTTGAGTGCTTGAAAT**TG**AGGAAGTGAAGAAATTAATTTCTCATGT
ATTTTTCTCATTTATTTATTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGA
TATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACA
TCAAACATTTATTTTTTTATTCTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGC
AGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTC
CACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCACTAATTTTTGTATTTT
TAGTAGAGACGGGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAAGTCTGGCCTCAAACAAT
CCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAA
ACATTTATCTTTTCTTTGTGTTGGGAACTTTGAAATTATACAATGAATTATTGTTAACTGTC
ATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTAC
CAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCA
TTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTGAGTAAGAAAATGCA
ATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATG
TTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

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FIGURE 212

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPLVSC
QPVKGHGTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 213

AGGGCCCGCGGGTGGAGAGAGCGACGCCGAGGGG**ATG**GCGGCAGCGTCCCGGAGCGCCTCT
GGCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGCCGGCTCCGGCGTCTT
CCAGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGCGTACTGGCCAGTGGGCGGCCTTGCG
AGCCCGGCTGCCGGAATTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTCTGTCTCGCCC
GGACCCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCG
GGACGACAGTAGCGGCGGGGGCGCAACCCTCTCCAAGTCCCTTCAATTTACCTGGCCGG
GTACCTTCTCGCTCATCATCGAAGCTTGGCAGCGGCCAGGAGACGACCTGCGGCCAGAGGCC
TTGCCACCAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGAGAA
CTGGTTATTGGATGAGCAAACCAGCACCTCACAAGGCTGCGCTACTCTTACCGGGTCTATCT
GCAGTGACAAGTACTATGGAGACAAGTCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTC
GGCCACTATGTGTGCCAGCCAGATGGCAACTTGTCTTGCCTGCCCGGTTGGACTGGGGAATA
TTGCCAACAGCCTATCTGTCTTTCGGGCTGTGATGAACAGAATGGCTACTGCAGCAAGCCAG
CAGAGTGCCTCTGCCGCCCAGGCTGGCAGGGCCGGCTGTGTAACGAATGCATCCCCACAAT
GGCTGTGCGCCACGGCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGG
CCTGTTTTGTGACCAAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAA
CGTGCTCCAACAGTGGGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTG
GACTGTGAGCTGGAGCTCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAA
GGACCAGGAGGATGGCTACCACTGCCTGTGTCTTCCGGGCTACTATGGCCTGCACTGTGAAC
ACAGCACCTTGAGCTGCGCCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAAC
CAGGGGGCCAACTATGCTTGTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAGAA
AGTGGACAGGTGCACCAGCAACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAA
GCCGCATGTGCCGCTGCCGTCTGGATTACGGGCACCTACTGTGAAGTCCACGTGAGCGAC
TGTGCCCCGTAACCCCTTGCGCCACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTG
CACCTGCCCCTGCCGGCTTCTCTGGCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTG
TGCAACTGCCCTTATGGCTTTGTGGGCAGCCGCTGCGAGTTCCTCGTGGGCTTGGCGCCAG
CTTCCCCTGGGTGGCCGTCTCGCTGGGTGTGGGGCTGGCAGTGCTGCTGGTACTGCTGGGCA
TGGTGGCAGTGGCTGTGCGGCAGCTGCGGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCC
ATGAACAAGTGTGCGGACTTCCAGAAGGACAACCTGATTCCTGCCGCCCAGCTTAAAAACAC
AAACCAGAAGAAGGAGCTGGAAGTGGACTGTGGCCTGGACAAGTCCAAGTGTGGCAAACAGC
AAAACCACACATTGGACTATAATCTGGCCCCAGGGCCCTGGGGCGGGGGACCATGCCAGGA
AAGTTTCCCCACAGTGACAAGAGCTTAGGAGAGAAGGCGCCACTGCGGTTACACAGTGAAAA
GCCAGAGTGTGGATATCAGCGATATGCTCCCCAGGGACTCCATGTACCAGTCTGTGTGT
TGATATCAGAGGAGAGGAATGAATGTGTGCTTGGCACGGAGGTAT**TAA**GGCAGGAGCCTACCT
GGACATCCCTGCTCAGCCCCGCGGCTGGACCTTCCTTCTGCATTGTTTACA

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FIGURE 214

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCL
 KHFAQVVSPPGCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHA
 PGDDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYGDNCSR
 LCKKRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGR
 LCNECIPHNGCRHGTCTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTC
 TCRPGYTGVDCLELSECDNPNCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCF
 NGGSCRERNQGANACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPPSRMCRCPGFTG
 TYCELHVSDCARNPCAAGGTCHDLENGLMCTCPAGFSGRRCVTSIDACASSPCFNRTCY
 TDLSTDTFVCNCPYGFVGSRCFPVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLR
 RPDDGSREAMNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPG
 PLGRGTM PGKFFHSDKSLGEKAPLRHLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIA
 TEV

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 530-552

N-glycosylation sites.

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

Glycosaminoglycan attachment site.

amino acids 96-100

Tyrosine kinase phosphorylation site.

amino acids 340-347

N-myristoylation sites.amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

Aspartic acid and asparagine hydroxylation site.

amino acids 339-351

EGF-like domain cysteine pattern signature.amino acids 173-185, 206-218, 239-251, 270-282, 310-322,
348-360, 388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394,
411-432, 449-470

FIGURE 215

[illegible]

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FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302**Myelin P0 protein.**

amino acids 96-125

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FIGURE 217

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
GGACCAGAAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTTCACTGCAAGTGCCTGCT
GTTCCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAG**ATG**AAAGCC
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
ATTTTTTTACTTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
AGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT
AGGGGGGTTATTCAATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAA

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FIGURE 218

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGN
IDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSELT
IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

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FIGURE 219

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCC
GCGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCCTGAGCCTCGGGCTCCGGCCCCGGAC
CTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGAT
GGCTTTAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCT
ATTTGTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGG
TCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGG
CTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACT
GGGGCTTCAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCA
AATTGTTTCAGCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGAC
GAAACTTGTGCGGCTTTCAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACG
AACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGG
GACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGTGGCCCTGCTCAT
CCTCTGTGTATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGT
CGCAGGACATTCAGTACAACGGCTCTGAGCTGTCGTGTTTGTGACAGACCTCAGTCCACGAA
TATGCCCACAGAGCCTGCTGCCAGTGCCGCGGTGACTCAGTGCAGACCTGCGGGCCGGTGCG
CTTGCTCCCATCCATGTGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTG
GGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCG
ACTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTAGATGCCTGGCCTCTGAT
GCAGAATCCCATGGGTGGTGACAACATCTCTTTTGTGACTCTTATCCTGAACTCACTGGAG
AAGACATTCAATCTCTCAATCCAGAAGTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGT
CAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTAC
TGATTTTATAGATATAACAACACACTGCTAGAATCAGCATCAACTCAGGATGCACTAACTA
TGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTC
CAGGAAGCTTAAAGAACCTGCTTCTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTA
CTCCTTTGTTAGGCTTATGGACTGAGCAGTCTGGACCTTGCAATGGCTTCTGGGGCAAAAATA
AATCTGAACCAAACCTGACGGCATTTGAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGC
TGTAAGCTGAAACCTCAATGAATAACAAGAAAAGACTCCAGGCCGACTCATGATACTCTGCA
TCTTTCCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACTGATGGGTGAGCT
GGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATGCTTATTTTCAT
GGTGATTGTGGTTTTTACAAGACTGAAGACCAGAGTATACTTTTTCTTCCAGAAATAATTT
CATAACGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAAGT
GAGTGTCTTCTATTTGAGAAGGACACTTTTTTCATCATCTAACTGATTCCCATAGGTGGTTAG
AATGGCCCTCATATTGCCTGCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAATCAGAG
GAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCCACACTTCTGACCTCAGCCTCGGTCTC
ATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGGAATGTGGTCGAGAAAGGGCAGC
CCATTGCCCAGAAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGGCATATTTATATG
AAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCCTCTGCCTGAGCTTAGAAGGTTAT
AGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGTATCTTATACTAAAGGC
TTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGTAGCCTTCCGTGAGAACACACC
ACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTTGGATGAAGCAGCTGTAAGT
CCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAATTGTGTAAGATTAGTTAGCA
CATCATCTCCTACTTTAGCCATCCGGTGTTGGATTTAAGAGGACGGTGCTTCTTTCTATTAA
AGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAGCTAAGACAGAAATTAAC
CCCGTTCACTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTTTATGCCCTGGAGAAGA
CCTACTTGAACAGGGCATATTTTTTTAGACTTCTGAACATCAGTATGTTTCGAGGGTACTATGA
TATTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTTAACTGAATATTAA
AATGTATCTGTCTTCTCT

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FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLEQEKTFFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHREFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDPPEPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCMCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids
1-25

Transmembrane domain:

Amino acids
169-192

N-glycosylation sites:

Amino acids
105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids
200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids
207-214

N-myristoylation sites:

Amino acids
55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids
259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids
89-96

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FIGURE 221

[illegible]

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FIGURE 222

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQS
KDYAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCF
TISTRPWMTQFSLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

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FIGURE 223

AATCGGCTGATTCTGCATCTGGAACTGCCTTCATCTTGAAAGAAAAGCTCCAGGTCCCT
TCTCCAGCCACCCAGCCCCAAGATGGTGATGCTGCTGCTGCTGCTTTCCGCACTGGCTGG
CCTCTTCGGTGCGGCAGAGGGACAAGCATTTCATCTTGGGAAGTGCCCCAATCCTCCGGT
GCAGGAGAATTTTGACGTGAATAAGTATCTCGGAAGATGGTACGAAATTGAGAAGATCCC
AACAACTTTGAGAATGGACGCTGCATCCAGGCCAACTACTCATAATGGAAAACGGAAA
GATCAAAGTGTTAAACCAGGAGTTGAGAGCTGATGGAAGTGTGAATCAAATCGAAGGTGA
AGCCACCCAGTTAACCTCACAGAGCCTGCCAAGCTGGAAGTTAAGTTTTCTGGTTTAT
GCCATCGGCACCGTACTGGATCCTGGCCACCGACTATGAGAACTATGCCCTCGTGTATTC
CTGTACCTGCATCATCCAACCTTTTTACGTGGATTTTGCTTGGATCTTGGCAAGAAACCC
TAATCTCCCTCCAGAAACAGTGGACTCTCTAAAAAATATCCTGACTTCTAATAACATTGA
TGTCAGAAAAATGACGGTCACAGACCAGGTGAACTGCCCCAAGCTCTCGTTAACCAGGTTT
TACAGGGAGGCTGCACCCACTCCATGTTACTTCTGCTTCGCTTTCCCCTACCCACCCCC
CCCCATAAAGACAAACCAATCAACCACGACAAAGGAAGTTGACCTGAACATGTAACCAT
GCCCTACCCTGTTACCTTGCTAGCTGCAAATAAACTTGTTGCTGACCTGCTGTGCTCGC
AAAAAA

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FIGURE 224

MVMLLLLLSALAGLFGAAEQAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTTFENG
RCIQANYSLMENGKIKVLNQELRADGTVNQIEGEATPVNLTEPAKLEVKFSWFMPSPAY
WILATDYENYALVYSCTCIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKM
TVTDQVNCPKLS

Signal sequence

1-16

N-glycosylation site.

65-68

98-101

cAMP- and cGMP-dependent protein kinase phosphorylation site.

175-178

N-myristoylation site.

13-18

16-21

Lipocalin proteins.

36-47

120-130

Lipocalin / cytosolic fatty-acid binding proteins

41-185

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FIGURE 225

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTG
CCTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGG
GCGTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACCATGTTCAAGGTAA
TTCAGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCA
AAAAAGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACTCTACTCAGTTCC
TGAGGGTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGC
TCCGACACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTA CTCCCAAACTAAGCCC
AAGATGCAAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCC
TGGATTTTTTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTA
GAGGTTCAAAAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTC
TATTATCCACAACAAGCCATCGTGTGTTGCCAGGTCAGTGGGGAGAGATTATATGACTGGGG
TTTACGAGGATATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATG
TGAAGAATTACCTGGAAC TAAGTAGAAAACCTCATGCTCTGCCATCTTAATCAGTTATAGG
TAAACATTGGAACTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAG
TATTGAATGTATTAAATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTT
CTGTGAAATCATCCTACAAGCAAATAACCTGGAATCCCTTCACCTAGAGATAATGTACAAG
CCTTAGAACTCCTCATTCTCATGTTGCTATTTATGTACCTAATTAAACCCAAGTTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 226

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEE
SISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIG
LLARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQ
KPGNVKNSPGTK

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195

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FIGURE 227

CACCGGAGGGGCACGCAGCTGACGGAGCTGCGCTGCGTTTCGCCTCGTTTGCCTCGCGCCCTCC
ACTGGAGCTGTTTCGCGCCTCCCGGCTCCACCCGCAGCCCACCCGGCAGAGGAGTCGCTACCA
GCGCCCAGTGCGCTCTGTCTAGTCCGCAAACCTCCTTGCCGCCCCGCCCCGGGCTGGGCACCAAA
TACCAGGCTACCAATGGTCTACAAGACTCTCTTCGCTCTTTGCATCTTAACTGCAGGATGGAG
GGTACAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCAC
CGACCACCATCTGGACTAGCTCTCCACAAACACTGATGCAGACACTGCCTCCCCATCCAAC
GGCACTCACAACAACCTCGGTGCTCCCAAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAA
GAACATTTCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTGAATTGGGAAGGCA
CAAACACAGACCCCTCACCTTCTGGGTTCTCGTCAACAAGCGGTGGAGTCCACTTAAACAACC
ACGTTGGAGGAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGCAGTC
CGCTGCTGAGCCTCCACACTCATCTCCCTCAAGCTCCAGCCTCATCACCTCATCCCTAT
CAACCTCACCACTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACC
AGCACCCAACCCACTGGAGCTCCAAGTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGA
CCACACACCCACTTCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAA
CTGTGTCTAGGCAAAGTGATGTGTGAGCTCATAGACATGGAGACCACCACCTTTCCCAGG
GTGATCATGCAGGAAGTAGAACATGCATTAAGTTCAGGCAGCATCGCCGCCATTACCGTGAC
AGTCATTGCCGTGGTGCTGCTGGTGTTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCTCT
CCTATGGAAGACTTTTGGACGACCATGACTACGGGTCTGGGGAACTACAACAACCTCTG
TACGATGACTCCTAACAATGGAATATGGCCTGGGATGAGGATTAAGTGTCTTTATTTATAA
GTGCTTATCCAGTAGAATTAATAAGTACCTGATGCGCATTGAACGACAATCTTAAGCCCTGT
TTTGTGTTGGTATGGTTGTTTTGTTTTCTCCCTCTCCTCTGGCTGCTACAACTTCCCCTTTC
TGGTACAAGAAGAACCATTCTTTAAAGGTGAGTGGAGGCTGATTGTCAGCTGAAGTGGGCCA
GCCTTGCACCAGCCAGGCCAGACCACCATGGTGAAGGCTTCTTCCCCACTGCAGGACCCAC
TTTGAGAAGGATCGAGGAGGAGGATTTGGGTTGTTTTGTTAGGGGTTACTTTCAGGGGAACA
TTTCATTTGTGTTATTTCTTAACTTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGA
AAGGAAATGAGCTCTACGAGGATTTACCTTGCATGGGAGAGAGCAGGGTTTTCTCAGATTCT
CTTTTTAATCTCTATTTATCTGGTTGTTTCTGACAGGATGCTGCCTGCTTGCTCTACGAGC
TGGAAGCAGCTTCTTAGCTGCCTAATTAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGG
GGCCAGCAGGTCACGGGGCAGAACTCTCTCAGGTTGCTGTGGGATCTCAGTGTGCCCTACCT
GTTCTCCCCTCCAGGCCACCTGTCTCTGTAAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGG
GATCCCAGCCCACAAGTGATCAGCAGAGTTGCATTTCCAAAGAAAAGGCTATGAGATGAGC
TGAGTTATAGAGAGAAAGGGAGAGGCATGTACGGTGTGGGGAAGTGGAAGAGAAGCTGGCGG
GGGAGAAGGAGGCTAACCTGCACTGAGTACTTCATTAGGACAAGTGAGAATCAGCTATTGAT
AATGGCCAGAGATATCCACAGCTTGGAGGAGCCCAGAGACTGTTTGCTTTATACCCACACAG
CAACTGGTCCACTGCTTTACTGTCTGTTGGATAATGGCTGTAAATGTTTAAAAAC

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FIGURE 228

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHN
NSVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEE
HSSGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQP
TGAPTAPESPTEESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTFPRVIMQ
EVEHALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPLYDDS

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 258-278

N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

Casein kinase II phosphorylation sites.

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

Tyrosine kinase phosphorylation site.

amino acids 289-296

N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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FIGURE 229

CTCCTGCACTAGGCTCTCAGCCAGGGATGATGCGCTGCTGCCGCCGCCGCTGCTGCTGCCGG
CAACCACCCCATGCCCTGAGGCCGTTGCTGTTGCTGCCCCCTCGTCCTTTTACCTCCCCTGGC
AGCAGCTGCAGCGGGCCCAACCGATGTGACACCATATACCAGGGCTTCGCCGAGTGTCTCA
TCCGCTTGGGGGACAGCATGGGCCGCGGAGGCGAGCTGGAGACCATCTGCAGGTCTTGGAAT
GACTTCCATGCCTGTGCCTCTCAGGTCCTGTCAGGCTGTCCGGAGGAGGCAGCTGCAGTGTG
GGAATCACTACAGCAAGAAGCTCGCCAGGCCCCCCCGTCCGAATAACTTGCACACTCTGTGCG
GTGCCCCGGTGATGTTCTGGGAGCGCGGCACAGGCTCCGAAACCAACCAGGAGACGCTGCGG
GCTACAGCGCCTGCACTCCCCATGGCCCCCTGCGCCCCCACTGCTGGCGGCTGCTCTGGCTCTG
GCCTACCTCCTGAGGCCTCTGGCCTAGCTTGTTGGGTTGGGTAGCAGCGCCCGTACCTCCAG
CCCTGCTCTGGCGGTGCTTGTCCAGGCTCTGCAGAGCGCAGCAGGGCTTTTCATTAAAGGTA
TTTATATTTGTA

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92265
><subunit 1 of 1, 165 aa, 1 stop
><MW: 17786, pI: 8.43, NX(S/T): 0
MMRCCRRRCCCRQPPHALRPLLLLPLVLLPPLAAAAAGPNRCDTIYQGFAECLIRLGDSM
GRGGELETICRSWNDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGAPVH
VRERGTGSETNQETLRATAPALPMAPAPPLLAALALAYLLRPLA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Transmembrane domain:

Amino acids 141-157

N-myristoylation site:

Amino acids 127-133

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 77-88

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FIGURE 231

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCCCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTGAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGAAAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGATTAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAA

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FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK
KGKIQQQELSAHQAPSPPAHSGFHRVYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

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FIGURE 233

AAGGAGCAGCCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACCTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCAGTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTAAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

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FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:
amino acids 1-18

N-glycosylation sites.
amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 102-106

N-myristoylation site.
amino acids 24-30

Actinin-type actin-binding domain signature 1.
amino acids 159-169

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FIGURE 235

GCCCCGGCGGGCTGCCCTTGGGTGCTCCCTTCCCTGCCCCGACACCCAGACCGACCTTGACCGC
CCACCTGGCAGGAGCAGGACAGGACGGCCGGACGCGGCCATGGCCGAGCTCCCGGGGGCCCTT
TCTCTGCGGGGCCCTGCTAGGCTTCCTGTGCCTGAGTGGGCTGGCCGTGGAGGTGAAGGTAC
CCACAGAGCCGCTGAGCACGCCCCCTGGGGAAGACAGCCGAGCTGACCTGCACCTACAGCACG
TCGGTGGGAGACAGCTTCGCCCTGGAGTGGAGCTTTGTGCAGCCTGGGAAACCCATCTCTGA
GTCCCATCCAATCCTGTACTTCACCAATGGCCATCTGTATCCAAGTGGTTCTAAGTCAAAGC
GGGTCAGCCTGCTTCAGAACCCCCCACAGTGGGGGTGGCCCACTGAAACTGACTGACGTC
CACCCCTCAGATACTGGAACCTACCTCTGCCAAGTCAACAACCCACCAGATTCTACACCAA
TGGGTGGGGCTAATCAACCTTACTGTGCTGGTTCCCCCAGTAATCCCTTATGCAGTCAGA
GTGGACAAACCTCTGTGGGAGGCTCTACTGCACTGAGATGCAGCTCTTCCGAGGGGGCTCCT
AAGCCAGTGTACAACCTGGGTGCGTCTTGGAACTTTTCTACACCTTCTCCTGGCAGCATGGT
TCAAGATGAGGTGTCTGGCCAGCTCATTCTACCAACCTCTCCCTGACCTCCTCGGGCACCT
ACCGCTGTGTGGCCACCAACCAGATGGGCAGTGCATCCTGTGAGCTGACCTCTCTGTGACC
GAACCCTCCCAAGGCCGAGTGGCCGGAGCTCTGATTGGGGTGCTCCTGGGCGTGCTGTTGCT
GTCAGTTGCTGCGTTCTGCCTGGTCAGGTTCCAGAAAGAGAGGGGGAAGAAGCCCAAGGAGA
CATATGGGGGTAGTGACCTTCGGGAGGATGCCATCGCTCCTGGGATCTCTGAGCACACTTGT
ATGAGGGCTGATTCTAGCAAGGGGTTCTTGGAAGACCCCTCGTCTGCCAGCACCGTGACGAC
CACCAAGTCCAAGCTCCCTATGGTTCGTGTGACTTCTCCCCGATCCCTGAGGGCGGTGAGGGGG
AATATCAATAATTAAAGTCTGTGGGTACCCTTNAAAAAAAAAAAA

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FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108760
><subunit 1 of 1, 327 aa, 1 stop
><MW: 34348, pI: 7.88, NX(S/T): 2
MAELPGPFLLCGALLGFLCLSGLAVEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFALEWS
FVQPGKPISESHPILYFTNGHLYPTGSKSKRVSLQLQNPPTVGVATLKLTDVHPSDTGTYL
CQVNNPPDFYTNGLGLINLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNWV
RLGTFPTPSPGSMVQDEVSGQLILTSLTSSGTYRCVATNQMGASCELTLSVTEPSQG
RVAGALIGVLLGVLLLSVAAFCLVRFOKERGKKPKETYGGSDLREDAIAPGISEHTCMRA
DSSKGFLERPSSASTVTTTKSKLPMVV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 242-260

N-glycosylation sites:

Amino acids 138-142;206-210

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 90-94

N-myristoylation sites:Amino acids 11-17;117-123;159-165;213-219;224-230;244-250;
248-254**Amidation site:**

Amino acids 270-274

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 218-229

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FIGURE 237

GGATGCAGCAGAGAGGAGCAGCTGGAAGCCGTGGCTGCGCTCTCTTCCCTCTGCTGGGCG
TCCTGTTCTTCCAGGGTGTTTATATCGTCTTTTCCTTGGAGATTCGTGCAGATGCCCCATG
TCCGAGGTTATGTTGGAGAAAAGATCAAGTTGAAATGCACTTTCAAGTCAACTTCAGATG
TCACTGACAAGCTTACTATAGACTGGACATATCGCCCTCCCAGCAGCAGCCACACAGTAT
CAATATTTTATTATCAGTCTTTCCAGTACCCAACCACAGCAGGCACATTTTCGGGATCGGA
TTTCTCTGGGTTGGAAATGTATACAAAGGGGATGCATCTATAAGTATAAGCAACCCCTACCA
TAAAGGACAATGGGACATTCAGCTGTGCTGTGAAGAATCCCCAGATGTGCACCATAATA
TTCCCATGACAGAGCTAACAGTCACAGAAAGGGGTTTTGGCACCATGCTTTCTCTGTGG
CCCTTCTTCCATCCTTGTCTTTGTGCCCTCAGCCGTGGTGGTTGCTCTGCTGCTGGTGA
GAATGGGGAGGAAGGCTGCTGGGCTGAAGAAGAGGAGCAGGTCTGGCTATAAGAAGTCAT
CTATTGAGGTTTTCCGATGACACTGATCAGGAGGAGGAAGAGGCGTGTATGGCGAGGCTTT
GTGTCCGTTGCGCTGAGTGCCTGGATTTCAGACTATGAAGAGACATATTGATGAAAGTCTG
TATGACACAAGAAGAGTCACCTAAAGACAGGAAACATCCCATTCCACTGGCAGCTAAAGC
CTGTCAGAGAAAGTGGAGCTGGCCTGGACCATAGCGATGGACAATCCTGGAGATCATCAG
TAAAGACTTTAGGAACCACTTATTTATTGAATAAATGTTCTTGTGTTGTTATTTATAAACTGT
TCAGGAAGTCTCATAAGAGACTCATGACTTCCCCTTTCAATGAATTATGCTGTAATTGAA
TGAAGAAATTCTTTTCCTGAGCA

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FIGURE 238

MQORGAAGSRGCALFPLLGVLFQGVYIVFSLEIRADAHVRGYVGEKIKLKCTFKSTSD
VTDKLTIDWTYRPFSSSHTVSIHYQSFOYPTTAGTFRDRISWVGNVYKGDASISINP
TIKDNGTFSCAVKNPPDVHHNIPMTLTVTERGFGTMLSSVALLSILVFVPSAVVVALL
LVRMGRKAAGLKKRSRSGYKKSSIEVSDDTDQEEEEACMARLCVRCAECLDSDYEETY

Transmembrane domain

11-30
157-177

N-glycosylation site

123-127

cAMP- and cGMP-dependent protein kinase phosphorylation site

189-193
197-201

Tyrosine kinase phosphorylation site

63-71

N-myristoylation site

5-11
8-14
124-130
153-159

Amidation site

181-185

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FIGURE 239

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCC
TCGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCTCTGTT
TGGGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAAATGGTGAACATAAAATGAAAGCAAGATTGAAGAGAT
GGTTGAACCACTAAGAGAGAAAAATCAGAGATTTAGAAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTT
TATCAGAAAAAGGATCGGAAAAAGATTTTGATAACAGGAGGCGCAGGGTTCTGTTGGGCTCCCATCTAACTGACAAA
CTCATGATGGACGGCCACGAGGTGACCGTGGTGACAATTTCTTCACGGGCAGGAAGAGAAAACGTGGAGCACTG
GATCGGACATGAGAACTTCGAGTTGATTAAACCACGACGTGGTGGAGCCCCCTCTACATCGAGGTTGACCAGATAT
ACCATCTGGCATCTCCAGCCTCCCCTCCAAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATT
GGGACATTAAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTA
TGGAGATCCTGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCT
ACGATGAAGGCAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGAAGTGCGAGTG
GCCAGAATCTTCAACACCTTTGGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCA
GGCGCTCCAGGGGGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTCAGCGATC
TAGTGAATGGCCTCGTGGCTCTCATGAACAGCAACGTCAGCAGCCCGGTCAACCTGGGGAACCCAGAAGAACAC
ACAATCCTAGAATTTGCTCAGTTAATTAACAACTTGTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGC
CCAGGATGACCCACAGAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCC
CGCTGGAGGAAGGTTTAAACAAAGCAATTCACACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTAC
ATCCCCAAACCAAAGCCTGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAAGTCTCTACTTTTAGGACAC
AAGACTACCATTGTACACTTGATGGGATGTATTTTGGCTTTTTTTTGTGTCGTTTAAAGAAAGACTTTAACA
GGTGTCTATGAAGAACAACCTGGAATTTCAATCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCC
TCAAAAACCTGCAGATTTTGCCTTGCACTTTTTGAATCTCTTTTTTATGTAAATAGCGTAGATGCATCTCTG
CGTATTTTCAAGTTTTTTTATCTTGCTGTGAGAGCATATGTTGTGACTGTGCTTACAGTTTTTATTTACTGGTT
TCTTTGTGAAGCTGAAAAGGAACATTAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAAT
AAATGAGTCGTTATACTATGCATAAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTT
TAGGGCAGATAAAAGAATTCTGTGTGAGAGCTTTATGTTTCTCTTTTAAATTCAGAGTTTTTCCAAGGTCTACTT
TTGAGTTGCAAACTTGACTTTGAAATATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTT
GCTGCGTATCTGGGGCGGGGCGAGGTTGGGGGCGACAAAGTTAACATATTCTTGTTAACCATGGTTAAATATG
CTATTTTAAATAAAATATTGAACTCA

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FIGURE 240

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPL
REKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTG
RKRNV EHWIGHENFELINHDVVEPLYIEVDQIYHLASPPNYMYPNPIKTLKTNITIGTLNM
LGLAKRVGARLLLASTSEVYGDPEVHPQSEDYWGHVNPIGPRACYDEGKRVAETMCYAYMKQ
EGVEVRVARIFNTFGPRMHMNDGRVVS NFILQALQGEPLTVYSGSQTRAFQYVSDLVNGLV
ALMNSNVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKLML
GWEPVVPLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41, 101-107, 383-389

Amidation sites:

amino acids 123-127, 233-237

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FIGURE 241

GCCCCGGTGGAGAATTAGGTGCTGCTGGGAGCTCCTGCCTCCCACAGGATTCCAGCTGCAGGG
AGCCTCAGGGACTCTGGGCCGCACGGAGTTGGGGGCATTCCCCAGAGAGCGTCGCC**ATGGTC**
TGCAGGGAGCAGTTATCAAAGAATCAGGTCAAGTGGGTGTTTGCCGGCATTACCTGTGTGTC
TGTGGTGGTCATTGCCGCAATAGTCCTTGCCATCACCTGCGGCGGCCAGGCTGTGAGCTGG
AGGCCTGCAGCCCTGATGCCGACATGCTGGACTACCTGCTGAGCCTGGGCCAGATCAGCCGG
CGAGATGCCTTGGAGGTCACCTGGTACCACGCAGCCAACAGCAAGAAAGCCATGACAGCTGC
CCTGAACAGCAACATCACAGTCCTGGAGGCTGACGTCAATGTAGAAGGGCTCGGCACAGCCA
ATGAGACAGGAGTTCCCATCATGGCACACCCCCCACTATCTACAGTGACAACACACTGGAG
CAGTGGCTGGACGCTGTGCTGGGCTCTTCCCAAAGGGCATCAAAGTGGACTTCAAGAACAT
CAAGGCAGTGGGGCCCTCCCTGGACCTCCTGCGGCAGCTGACAGAGGAAGGCAAAGTCCGGC
GGCCCATATGGATCAACGCTGACATCTTAAAGGGCCCCAACATGCTCATCTCAACTGAGGTC
AATGCCACACAGTTCTTGGCCCTGGTCCAGGAGAAGTATCCCAAGGCTACCTATCTCCAGG
CTGGACCACCTTCTACATGTCCACGTCCCCAAACAGGACGTACACCCAAGCCATGGTGGAGA
AGATGCACGAGCTGGTGGGAGGAGTGGCCAGAGGGTCACCTTCCCTGTACGGTCTTCCATG
GTGCGGGCTGCCTGGCCCCACTTCAGCTGGCTGCTGAGCCAATCTGAGAGGTACAGCCTGAC
GCTGTGGCAGGCTGCCTCGGACCCCATGTGGTGGAAGATCTGCTCTACGTCCGGGATAACA
CTGCTGTCCACCAAGTCTACTATGACATCTTTGAGCCTCTCCTGTACAGTTCAAGCAGCTG
GCCTTGAATGCCACACGGAAACCAATGTACTACACGGGAGGCAGCCTGATCCCTCTTCTCCA
GCTGCCTGGGGATGACGGTCTGAATGTGGAGTGGCTGGTTCCTGACGTCCAGGGCAGCGGTA
AAACAGCAACAATGACCCCTCCAGACACAGAAGGCATGATCCTGCTGAACACTGGCCTCGAG
GGAAGTGTGGCTGAAAACCCCGTGCCCATTTGTTCACTCCAAGTGGCAACATCCTGACGCT
GGAGTCTTGCCTGCAGCAGCTGGCCACACATCCCGGACACTGGGGCATCCATTTGCAAATAG
TGGAGCCCGCAGCCCTCCGGCCATCCCTGGCCTTGCTGGCACGCCTCTCCAGCCTTGGCCTC
TTGCATTGGCCTGTGTGGGTTGGGGCCAAATCTCCACGGGAGTTTTTCGGTCCCCGGCCA
TGTGGCTGGCAGAGAGCTGCTTACAGCTGTGGCTGAGGTCTTCCCCACGTGACTGTGGCAC
CAGGCTGGCCTGAGGAGGTGCTGGGCAGTGGCTACAGGGAACAGCTGCTCACAGATATGCTA
GAGTTGTGCCAGGGGCTCTGGCAACCTGTGTCTTCCAGATGCAGGCCATGCTGCTGGGCCA
CAGCACAGCTGGAGCCATAGGCAGGCTGCTGGCATCCTCCCCCGGGCCACCGTCACAGTGGAG
CACAACCCAGCTGGGGGCGACTATGCCTCTGTGAGGACAGCATTGCTGGCAGCTAGGGCTGT
GGACAGGACCCGAGTCTACTACAGGCTACCCAGGGCTACCACAAGGACTTGCTGGCTCATG
TTGGTAGAAAT**TGAG**CACCCAGGGGTGGTGGGCCAGCGGACCTCAGGGCGGAGGCTTCCAC
GGGGAGGCAGGAAGAAATAAAGGTCTTTGGCTTTCTCCAGGCCAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119514
><subunit 1 of 1, 585 aa, 1 stop
><MW: 64056, pI: 6.58, NX(S/T): 5
MVCREQLSKNQVKWVFAGITCVSVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG
QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNV EGLGTANETGVPIMAHPTIY
SDNTLEQWLDAVLGSSQKGIKLD FKNIAVGPSLDLLRQLTEEGKVR RPIWINADILKGP
NMLISTEVNATQFLALVQEKYPKATLSPGWTFY MSTSPNRTYTQAMVEKMH ELVGGVQP
RVTFFVRSSMVRAAWPHFSWLLSQSERYS LTLWQAASDPMSVEDLLYVRDNTAVHQVYYD
IFEPLLSQFKQLALNATRKP MYTGGSLIPLLQLPGDDGLNVEWLVPDVQGS GKTATMTL
PDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLESC LQQLATHPGHWGIHLQIVEPAA
LRPSLALLARLSSLG LLHWPVWVGAKISHGSFSVPGHVAGRELLTAVAEVFP HVTVPAGW
PEEVLGSGYREQLLTDMLELCQGLWQPVSFQM QAMLLGHSTAGAIGRLLASSPRATVTVE
HNPAGGDYASVRTALLAARAVDRTRVYYRLPQGYHKDLLAHVGRN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 18-37 (Possible type II)

N-glycosylation sites:

Amino acids 89-93;106-110;189-193;220-224;315-319

Tyrosine kinase phosphorylation site:

Amino acids 65-74

N-myristoylation sites:

Amino acids 101-107;351-357;372-378;390-396;444-450;545-551

Aminotransferases class-V pyridoxal-phosphate attachment site:

Amino acids 312-330

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FIGURE 243

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTT
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAAGGAAGATGGGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTCAATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGCTTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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FIGURE 244

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 10/17800

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 B01D39/16

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 B01D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 4 215 682 A (DAVIS CHARLES I ET AL) 5 August 1980 (1980-08-05) column 6, line 23 - line 31; figure 4	1,2,7,9
Y	US 5 645 627 A (LIFSHUTZ NORMAN ET AL) 8 July 1997 (1997-07-08) Summary of the invention column 4, paragraph 2 - paragraph 3 column 6, paragraph 2 - paragraph 3	1,2,7,9

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

A document member of the same patent family

Date of the actual completion of the international search

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Fax (+31-70) 340-3016

Authorized officer

Plaka, T

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Information on patent family members

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		AT 82779 A	15-08-1985
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		AU 4391279 A	06-09-1979
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33/68, 33/574

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(72) Inventors; and

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09/816,744	22 March 2001 (22.03.2001)	US
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09/854,280	10 May 2001 (10.05.2001)	US

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NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
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Published:

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[Continued on next page]

WO 01/093983 A1

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.



(48) Date of publication of this corrected version:

12 December 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(15) Information about Correction:

see PCT Gazette No. 50/2002 of 12 December 2002, Section II

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

15 Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci. 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

25 Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

15 In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

20 In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%
25 alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1B show a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO6004 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA92259".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figures 1A-1B.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO4981 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA94849-2960".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO7174 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA96883-2745".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO5778 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA96894-2675".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4332 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA100272-2969".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO9799 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA108696-2966".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO9909 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA117935-2801".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO9917 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA119474-2803".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO9771 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA119498-2965".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO9877 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA119502-2789".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO9903 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA119516-2797".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO9830 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA119530-2968".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO7155 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA121772-2741".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO9862 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA125148-2782".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO9882 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA125150-2793".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO9864 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA125151-2784".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO10013 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA125181-2804".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO9885 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA125192-2794".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO9879 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA125196-2792".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO10111 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA125200-2810".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO9925 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA125214-2814".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO9905 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA125219-2799".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO10276 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA128309-2825".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO9898 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA129535-2796".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO9904 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA129549-2798".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO19632 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA129580-2863".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO19672 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA129794-2967".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO9783 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA131590-2962".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO10112 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA135173-2811".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figures 59A-59B show a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO10284 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA138039-2828".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figures 59A-59B.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO10100 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA139540-2807".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO19628 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA139602-2859".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO19684 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA139632-2880".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO10274 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA139686-2823".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO9907 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA142392-2800".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO9873 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA143076-2787".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO10201 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA143294-2818".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO10200 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA143514-2817".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO10196 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA144841-2816".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO10282 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA148380-2827".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO19650 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA149995-2871".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO21184 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA167678-2963".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO21201 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA168028-2956".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO21175 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA173894-2947".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO21340 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA176775-2957".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO21384 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA177313-2982".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO982 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA57700-1408".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO1160 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA62872-1509".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1187 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA62876-1517".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA66660-1585".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO231 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA34434-1139".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO357 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA44804-1248".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO725 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA52758-1399".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA59849-1504".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1306 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA65410-1569".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA71290-1630".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO229 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA33100-1159".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1272 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA64896-1539".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4405 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84920-2614".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO181 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA23330-1390".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO214 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA32286-1191".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO247 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA35673-1201".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO337 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA43316-1237".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO526 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA44184-1319".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO363 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA45419-1252".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO531 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA48314-1320".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA50921-1458".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO840 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA53987".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56047-1456".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO788 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56405-1357".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56531-1648".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56865-1491".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO826 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA57694-1341".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1005 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA57708-1411".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO809 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA57836-1338".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA57841-1522".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA58847-1383".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA59212-1627".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA59588-1571".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1025 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA59622-1334".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA59847-2510".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA60615-1483".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA60621-1516".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA62814-1521".

10 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1244 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA64883-1526".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA64889-1541".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1412 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA64897-1628".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA64903-1553".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1330 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA64907-1163-1".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1347 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA64950-1590".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA64952-1568".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA65402-1540".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA65405-1547".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1340 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA66663-1598".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA66667".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA66675-1587".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1376 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA67300-1605".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA68872-1620".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA71269-1621".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1488 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA73736-1657".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA73739-1645".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA76400-2528".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA76532-1702".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA76541-1675".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA79862-2522".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA81754-2532".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA81761-2583".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO5723 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA82361".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA83500-2506".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA84210-2576".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO3543 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA86571-2551".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO3444 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA87997".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA92218-2554".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA92223-2567".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO5725 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA92265-2669".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO4408 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA92274-2617".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO9940 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA92282".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO7154 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA108760-2740".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO7425 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA108792-2753".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA111750-2706".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO9836 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA119514-2772".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA125185-2806".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

15 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein
20 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO
25 polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide"
30 specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in
35 bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino

acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

5 The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1 % of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5 % of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

10 The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

20 "PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80 % amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80 % amino acid sequence identity, alternatively at least about 81 % amino acid sequence identity, alternatively at least about 82 % amino acid sequence identity, alternatively at least about 83 % amino acid sequence identity, alternatively at least about 84 % amino acid sequence identity, alternatively at least about 85 % amino acid sequence identity, alternatively at least about 86 % amino acid sequence identity, alternatively at least about 87 % amino acid sequence identity, alternatively at least about 88 % amino acid sequence identity, alternatively at least about 89 % amino acid sequence identity, alternatively at least about 90 % amino acid sequence identity, alternatively at least about 91 % amino acid sequence identity, alternatively at least about 92 % amino acid sequence identity, alternatively at least about 93 % amino acid sequence identity, alternatively at least about 94 % amino acid

sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

5 "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed
 10 herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid
 15 sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95%
 20 nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or
 25 without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120
 30 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences
 35 identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent

nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against

which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated

polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that:

- (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still

capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H - V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing

conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

5 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

10 By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a
15 discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

20 A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

25

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
5  * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10 int    _day[26][26] = {
/*    A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */    { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */    { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */    {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */    { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */    { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */    {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */    { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */    {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */    {-1, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */    {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */    {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */    {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */    { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */    {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */    { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */    { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */    {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */    { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */    { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */    { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */    {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */    {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */    { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};
40

45

50

55

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
15
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
20
    short          n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int            score;      /* score at last jmp */
    long           offset;     /* offset of prev block */
    short          ijmp;       /* current jmp index */
    struct jmp      jp;        /* list of jmps */
};

30
struct path {
    int            spc;        /* number of leading spaces */
    short          n[JMPS]; /* size of jmp (gap) */
    int            x[JMPS]; /* loc of jmp (last elem before gap) */
35
};

char            *ofile;      /* output file name */
char            *namex[2];   /* seq names: getseqs() */
char            *prog;       /* prog name for err msgs */
char            *seqx[2];    /* seqs: getseqs() */
40
int             dmax;         /* best diag: nw() */
int             dmax0;        /* final diag */
int             dna;          /* set if dna: main() */
int             endgaps;      /* set if penalizing end gaps */
int             gapx, gapy;    /* total gaps in seqs */
45
int             len0, len1;    /* seq lens */
int             ngapx, ngapy;  /* total size of gaps */
int             smax;         /* max score: nw() */
int             *xbm;         /* bitmap for matching */
long            offset;       /* current offset in jmp file */
50
struct          diag          *dx; /* holds diagonals */
struct          path          pp[2]; /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();
55

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5 * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
10 *
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
15 #include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};
20
static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25 1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                main
30     int    ac;
     char    *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
         fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
         fprintf(stderr, "The sequences can be in upper- or lower-case\n");
         fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
         fprintf(stderr, "Output is in the file \"align.out\"\n");
         exit(1);
40     }
     namex[0] = av[1];
     namex[1] = av[2];
     seqx[0] = getseq(namex[0], &len0);
     seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

     endgaps = 0;                                /* 1 to penalize endgaps */
     ofile = "align.out";                        /* output file */

50     nw();                                /* fill in the matrix, get the possible jumps */
     readjumps();                            /* get the actual jumps */
     print();                                /* print stats, alignment */

     cleanup(0);                                /* unlink any tmp files */
55 }

```

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
5 * a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
10     char *      *px, *py;          /* seqs and ptrs */
        int      *ndely, *dely;     /* keep track of dely */
        int      ndelx, delx;       /* keep track of delx */
        int      *tmp;             /* for swapping row0, row1 */
        int      mis;              /* score for each type */
15     int      ins0, ins1;          /* insertion penalties */
        register id;               /* diagonal index */
        register ij;              /* jmp index */
        register *col0, *col1;     /* score for curr, last row */
        register xx, yy;           /* index into seqs */
20
        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
25     col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

30     smax = -10000;
        if (endgaps) {
            for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                col0[yy] = dely[yy] = col0[yy-1] - ins1;
                ndely[yy] = yy;
35             }
            col0[0] = 0;          /* Waterman Bull Math Biol 84 */
        }
        else
40             for (yy = 1; yy <= len1; yy++)
                dely[yy] = -ins0;

        /* fill in match matrix
        */
45     for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
50                 col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
55             col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
60
    }

```

Table 1 (cont')

...nw

```

5      for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

10      /* update penalty for del in x seq;
        * favor new del over ongong del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
15             if (col0[yy] - ins0 >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
20            }
        } else {
            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
25            } else
                ndely[yy]++;
        }

        /* update penalty for del in y seq;
30        * favor new del over ongong del
        */
        if (endgaps || ndelx < MAXGAP) {
            if (col1[yy-1] - ins0 >= delx) {
35                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else {
                delx -= ins1;
                ndelx++;
            }
40        } else {
            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else
45                ndelx++;
        }

        /* pick the maximum score; we're favoring
50        * mis over any del and delx over dely
        */

```

55

60

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
5   else if (delx >= dely[yy]) {
        coll[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
            dx[id].jp.n[ij] = ndelx;
            dx[id].jp.x[ij] = xx;
            dx[id].score = delx;
        }
        else {
            coll[yy] = dely[yy];
            ij = dx[id].ijmp;
25      if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
            && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                    writejumps(id);
                    ij = dx[id].ijmp = 0;
                    dx[id].offset = offset;
                    offset += sizeof(struct jmp) + sizeof(offset);
                }
            }
            dx[id].jp.n[ij] = -ndely[yy];
            dx[id].jp.x[ij] = xx;
            dx[id].score = dely[yy];
        }
        if (xx == len0 && yy < len1) {
40          /* last col
            */
            if (endgaps)
                coll[yy] -= ins0+ins1*(len1-yy);
            if (coll[yy] > smax) {
45              smax = coll[yy];
              dmax = id;
            }
        }
    }
50   if (endgaps && xx < len0)
        coll[yy-1] -= ins0+ins1*(len0-xx);
    if (coll[yy-1] > smax) {
        smax = coll[yy-1];
        dmax = id;
55   }
    tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
60  (void) free((char *)col0);
    (void) free((char *)coll);
}

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3   /* space between name or num and seq */

20 extern _day[26][26];
int      olen;      /* set output line length */
FILE     *fx;       /* output file */

25 print()                                                    print
{
    int      lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
55     getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int      lx, ly;
    int      firstgap, lastgap;
    {
        int      nm, i0, i1, siz0, siz1;
10      char      outx[32];
        double    pct;
        register  n0, n1;
        register char *p0, *p1;

15      /* get total matches, score
        */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
        p1 = seqx[1] + pp[0].spc;
20      n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;

        nm = 0;
        while ( *p0 && *p1 ) {
25             if (siz0) {
                    p1++;
                    n1++;
                    siz0--;
            }
            else if (siz1) {
30                 p0++;
                    n0++;
                    siz1--;
            }
            else {
35                 if (xbm[*p0-'A']&xbm[*p1-'A'])
                        nm++;
                    if (n0++ == pp[0].x[i0])
                        siz0 = pp[0].n[i0++];
40                 if (n1++ == pp[1].x[i1])
                        siz1 = pp[1].n[i1++];
                    p0++;
                    p1++;
            }
45         }

        /* pct homology:
        * if penalizing endgaps, base is the shorter seq
        * else, knock off overhangs and take shorter core
        */
50      if (endgaps)
            lx = (len0 < len1)? len0 : len1;
        else
            lx = (lx < ly)? lx : ly;
55      pct = 100.*(double)nm/(double)lx;
      fprintf(fx, "\n");
      fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
            nm, (nm == 1)? "" : "es", lx, pct);
60

```

Table 1 (cont')

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? ":" : "s");
    fprintf(fx, "%s", outx);
}

fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapy, (dna)? "base":"residue", (ngapy == 1)? ":" : "s");
    fprintf(fx, "%s", outx);
}
if (dna)
    fprintf(fx,
        "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
    fprintf(fx,
        "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINS0, PINS1);
if (endgaps)
    fprintf(fx,
        "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (dna)? "base" : "residue", (firstgap == 1)? ":" : "s",
        lastgap, (dna)? "base" : "residue", (lastgap == 1)? ":" : "s");
else
    fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char  *ps[2];      /* ptr to current element */
static char  *po[2];      /* ptr to next output char slot */
static char  out[2][P_LINE]; /* output line */
static char  star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seq[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25            po[i]++;
            ps[i]++;

            /*
            * are we at next gap for this seq?
            */
30            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                * we need to merge all gaps
                * at this location
                */
35                siz[i] = pp[i].n[ij[i]] + +;
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]] + +;
            }
            ni[i]++;
40        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
50    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

```

...pr_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15     }
    }
}

/*
20  * put out a number line: dumpblock()
  */
static
nums(ix)
25  {
    int      ix;      /* index in out[] holding seq line */
    char      nline[P_LINE];
    register  i, j;
    register char *pn, *px, *py;
30
    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
35        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
40                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
45                i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
50    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

55 /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
static
putline(ix)
60  int      ix;      {

```

nums

putline

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
   {
       int          i;
       register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
           return;
       px = star;
       for (i = lmax+P_SPC; i; i--)
35         *px++ = ' ';

       for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
           if (isalpha(*p0) && isalpha(*p1)) {
40               if (xbm[*p0-'A']&xbm[*p1-'A']) {
                   cx = '*';
                   nm++;
               }
               else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                   cx = '.';
               else
                   cx = ' ';
           }
           else
50               cx = ' ';
           *px++ = cx;
       }
       *px++ = '\n';
       *px = '\0';
55  }

```

stars

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20

25

30

35

40

45

50

55

60

```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>
10
char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jumps */
FILE    *fj;

int      cleanup();                          /* cleanup tmp file */
15 long    lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                                cleanup
{
    int    i;
    if (fj)
        (void) unlink(jname);
25    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30
char    *
getseq(file, len)                                getseq
35 {
    char    *file;    /* file name */
    int     *len;     /* seq len */
    {
        char    line[1024], *pseq;
        register char    *px, *py;
        int     natgc, tlen;
        FILE    *fp;

        if ((fp = fopen(file, "r")) == 0) {
            fprintf(stderr, "%s: can't read %s\n", prog, file);
            exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
            if (*line == ';' || *line == '<' || *line == '>')
                continue;
            for (px = line; *px != '\n'; px++)
                if (isupper(*px) || islower(*px))
                    tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
            fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
            exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

...getseq

```

5      py = pseq + 4;
      *len = tlen;
      rewind(fp);

10     while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++) {
15             if (isupper(*px))
                *py++ = *px;
            else if (islower(*px))
                *py++ = toupper(*px);
            if (index("ATGCU", *(py-1)))
                natgc++;
        }
        *py++ = '\0';
        *py = '\0';
20     (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
    }

25     char *
    g_calloc(msg, nx, sz)
        char *msg;          /* program, calling routine */
        int nx, sz;         /* number and size of elements */
    {
30         char *px, *calloc();

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
            if (*msg) {
35                 fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                exit(1);
            }
        }
        return(px);
    }

40     /*
    * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
    */

    readjmps()
45     {
        int fd = -1;
        int siz, i0, i1;
        register i, j, xx;

50         if (fj) {
            (void) fclose(fj);
            if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                fprintf(stderr, "%s: can't open() %s\n", prog, jname);
                cleanup(1);
55             }
        }
        for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
            while (1) {
60                 for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                    ;
            }
        }
    }

```

g_calloc

readjmps

Table 1 (cont')**...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
10    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) {
20            /* gap in second seq */
            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
            */
            pp[1].x[i1] = xx - dmax + len1 - 1;
25            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
40    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
60    offset = 0;
    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5 writejumps(ix)                                     writejumps
    int    ix;
    {
        char    *mktemp();
10        if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15            if ((fj = fopen(jname, "w")) == 0) {
                fprintf(stderr, "%s: can't write %s\n", prog, jname);
                exit(1);
            }
20            (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
            (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
        }
25
30
35
40
45
50
55
60

```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXXX	(Length = 10 amino acids)
15 Comparison Protein	XXXXXXXXYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Table 4

25

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

20 As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

30 In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35 Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO
15 polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,3-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesei* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* 15 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolytocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not 20 limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant 25 cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, 30 ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

15 Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

20 Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

35 Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

5 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

10 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

15 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

20 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

25 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

30 Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for

a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection,

electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based

assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective

genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically

acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single

Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

5 The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

10 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

15 The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

20 In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

30 If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers

(Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are

prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

15 F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate
25 the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

30

2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an
35 immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally,

either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal

antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences

of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

5 Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of
10 human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10,
15 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10
20 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding
25 specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of
30 the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

35 Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the

first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar
10 size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically
15 cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized
25 bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by
35 Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on

the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared.

5 Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms
10 to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

15 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using
20 known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

25 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176:
30 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design,
35 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, **238**: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, **82**: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, **77**: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., **257**: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., **81**(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

5 If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See,
10 *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in
15 amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques
20 are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include
25 polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.
30 While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered
35 to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linker with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (*e.g.*, SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2×10^6 cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10^7 cells/ml (approx. OD₆₀₀=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μ g, vol. < 10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l Klentaq (Clontech, Palo Alto, CA); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:245)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:246)

PCR was then performed as follows:

- | | | |
|----|--------------|------------------|
| a. | Denature | 92°C, 5 minutes |
| b. | 3 cycles of: | |
| | Denature | 92°C, 30 seconds |
| | Anneal | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA94849-2960	PTA-2306	July 25, 2000
	DNA96883-2745	PTA-544	August 17, 1999
5	DNA96894-2675	PTA-260	June 22, 1999
	DNA100272-2969	PTA-2299	July 25, 2000
	DNA108696-2966	PTA-2315	August 1, 2000
	DNA117935-2801	PTA-1088	December 22, 1999
	DNA119474-2803	PTA-1097	December 22, 1999
10	DNA119498-2965	PTA-2298	July 25, 2000
	DNA119502-2789	PTA-1082	December 22, 1999
	DNA119516-2797	PTA-1083	December 22, 1999
	DNA119530-2968	PTA-2396	August 8, 2000
	DNA121772-2741	PTA-1030	December 7, 1999
15	DNA125148-2782	PTA-955	November 16, 1999
	DNA125150-2793	PTA-1085	December 22, 1999
	DNA125151-2784	PTA-1029	December 7, 1999
	DNA125181-2804	PTA-1096	December 22, 1999
	DNA125192-2794	PTA-1086	December 22, 1999
20	DNA125196-2792	PTA-1091	December 22, 1999
	DNA125200-2810	PTA-1186	January 11, 2000
	DNA125214-2814	PTA-1270	February 2, 2000
	DNA125219-2799	PTA-1084	December 22, 1999
	DNA128309-2825	PTA-1340	February 8, 2000
25	DNA129535-2796	PTA-1087	December 22, 1999
	DNA129549-2798	PTA-1099	December 22, 1999
	DNA129580-2863	PTA-1584	March 28, 2000
	DNA129794-2967	PTA-2305	July 25, 2000
	DNA131590-2962	PTA-2297	July 25, 2000
30	DNA135173-2811	PTA-1184	January 11, 2000
	DNA138039-2828	PTA-1343	February 8, 2000
	DNA139540-2807	PTA-1187	January 11, 2000
	DNA139602-2859	PTA-1588	March 28, 2000
	DNA139632-2880	PTA-1629	April 4, 2000
35	DNA139686-2823	PTA-1264	February 2, 2000
	DNA142392-2800	PTA-1092	December 22, 1999
	DNA143076-2787	PTA-1028	December 7, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA143294-2818	PTA-1182	January 11, 2000
	DNA143514-2817	PTA-1266	February 2, 2000
	DNA144841-2816	PTA-1188	January 11, 2000
5	DNA148380-2827	PTA-1181	January 11, 2000
	DNA149995-2871	PTA-1971	May 31, 2000
	DNA167678-2963	PTA-2302	July 25, 2000
	DNA168028-2956	PTA-2304	July 25, 2000
	DNA173894-2947	PTA-2108	June 20, 2000
10	DNA176775-2957	PTA-2303	July 25, 2000
	DNA177313-2982	PTA-2251	July 19, 2000
	DNA57700-1408	203583	January 12, 1999
	DNA62872-1509	203100	August 4, 1998
	DNA62876-1517	203095	August 4, 1998
15	DNA66660-1585	203279	September 22, 1998
	DNA34434-1139	209252	September 16, 1997
	DNA44804-1248	209527	December 10, 1997
	DNA52758-1399	209773	April 14, 1998
	DNA59849-1504	209986	June 16, 1998
20	DNA65410-1569	203231	September 15, 1998
	DNA71290-1630	203275	September 22, 1998
	DNA33100-1159	209377	October 16, 1997
	DNA64896-1539	203238	September 9, 1998
	DNA84920-2614	203966	April 27, 1999
25	DNA23330-1390	209775	April 14, 1998
	DNA32286-1191	209385	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA43316-1237	209487	November 21, 1997
	DNA44184-1319	209704	March 26, 1998
30	DNA45419-1252	209616	February 5, 1998
	DNA48314-1320	209702	March 26, 1998
	DNA50921-1458	209859	May 12, 1998
	DNA53987	209858	May 12, 1998
	DNA56047-1456	209948	June 9, 1998
35	DNA56405-1357	209849	May 6, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	DNA57694-1341	203017	June 23, 1998
	DNA57708-1411	203021	June 23, 1998
	DNA57836-1338	203025	June 23, 1998
	DNA57841-1522	203458	November 3, 1998
5	DNA58847-1383	209879	May 20, 1998
	DNA59212-1627	203245	September 9, 1998
	DNA59588-1571	203106	August 11, 1998
	DNA59622-1334	209984	June 16, 1998
	DNA59847-2510	203576	January 12, 1999
10	DNA60615-1483	209980	June 16, 1998
	DNA60621-1516	203091	August 4, 1998
	DNA62814-1521	203093	August 4, 1998
	DNA64883-1526	203253	September 9, 1998
	DNA64889-1541	203250	September 9, 1998
15	DNA64897-1628	203216	September 15, 1998
	DNA64903-1553	203223	September 15, 1998
	DNA64907-1163-1	203242	September 9, 1998
	DNA64950-1590	203224	September 15, 1998
	DNA64952-1568	203222	September 15, 1998
20	DNA65402-1540	203252	September 9, 1998
	DNA65405-1547	203476	November 17, 1998
	DNA66663-1598	203268	September 22, 1998
	DNA66667	203267	September 22, 1998
	DNA66675-1587	203282	September 22, 1998
25	DNA67300-1605	203163	August 25, 1998
	DNA68872-1620	203160	August 25, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA73736-1657	203466	November 17, 1998
	DNA73739-1645	203270	September 22, 1998
30	DNA76400-2528	203573	January 12, 1999
	DNA76532-1702	203473	November 17, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA79862-2522	203550	December 22, 1998
	DNA81754-2532	203542	December 15, 1998
35	DNA81761-2583	203862	March 23, 1999
	DNA83500-2506	203391	October 29, 1998
	DNA84210-2576	203818	March 2, 1999

Table 7 (cont')

	DNA86571-2551	203660	February 9, 1999
	DNA92218-2554	203834	March 9, 1999
	DNA92223-2567	203851	March 16, 1999
	DNA92265-2669	PTA-256	June 22, 1999
5	DNA92274-2617	203971	April 27, 1999
	DNA108760-2740	PTA-548	August 17, 1999
	DNA108792-2753	PTA-617	August 31, 1999
	DNA111750-2706	PTA-489	August 3, 1999
	DNA119514-2772	PTA-946	November 9, 1999
10	DNA125185-2806	PTA-1031	December 7, 1999

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

EXAMPLE 5: Isolation of cDNA clones Encoding Human PRO6004, PRO5723, PRO3444, and PRO9940

DNA molecules encoding the PRO840, PRO1338, PRO6004, PRO5723, PRO3444, and PRO9940 polypeptides shown in the accompanying figures were obtained through GenBank.

EXAMPLE 6: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe. DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following

high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

5 DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 7: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

10 The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated
15 into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA
20 sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

25 After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA
30 encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.₆₀₀ of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared
35 by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g

Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO_4) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

5 *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

15 The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

25 Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in mammalian cells

35 This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector.

Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

5 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

10 Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ^{35}S -cysteine and 200 μ Ci/ml ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

15 In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompayrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris.

20 The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

25 In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

30 Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells

can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

5 Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

10 Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits
15 selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect* (Qiagen), Dosper* or Fugene* (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

20 The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is
25 sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately
30 loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is

pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

- 5 Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently
10 desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Yeast

- 15 The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal
20 peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with
25 Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

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EXAMPLE 10: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

- The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG).
35 A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding

the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 11: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with

additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 12: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration

of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 13: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed
5 in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO
10 polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the
15 cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art.
25 Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide
30 which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 14: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson,
35

Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 15: Pericyte c-Fos Induction (Assay 93)

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 μ l of PRO polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM + 5% FBS.

The following polypeptides tested positive in this assay: PRO982, PRO1160, PRO1187, and PRO1329.

EXAMPLE 16: Chondrocyte Re-differentiation Assay (Assay 110)

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs.

5 The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined.

10 A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO357.

EXAMPLE 17: Identification of PRO Polypeptides That Stimulate TNF-α Release In Human Blood (Assay 128)

15 This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF-α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF-α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF-α release would be beneficial. Specifically, 200 µl of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300µl of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50µl of plasma is collected from each well and tested for the presence of TNF-α by ELISA assay. A positive in the assay is a higher amount of TNF-α in the PRO polypeptide treated samples as compared to the negative control samples.

25 The following PRO polypeptides tested positive in this assay: PRO231, PRO357, PRO725, PRO1155, PRO1306, and PRO1419.

EXAMPLE 18: Promotion of Chondrocyte Redifferentiation (Assay 129)

30 This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

35 Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control)

or the test PRO polypeptide are added to give a final volume of 200 μ l/well. After 5 days at 37°C, 22 μ l of media containing 100 μ g/ml Hoechst 33342 and 50 μ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

The following PRO polypeptides tested positive in this assay: PRO229, PRO1272, and PRO4405.

EXAMPLE 19: Normal Human Dermal Fibroblast Proliferation (Assay 141)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce proliferation of human dermal fibroblast cells in culture and, therefore, function as useful growth factors.

On day 0, human dermal fibroblast cells (from cell lines, maximum of 12-14 passages) were plated in 96-well plates at 1000 cells/well per 100 microliter and incubated overnight in complete media [fibroblast growth media (FGM, Clonetics), plus supplements: insulin, human epithelial growth factor (hEGF), gentamicin (GA-1000), and fetal bovine serum (FBS, Clonetics)]. On day 1, complete media was replaced by basal media [FGM plus 1% FBS] and addition of PRO polypeptides at 1%, 0.1% and 0.01%. On day 7, an assessment of cell proliferation was performed by Alamar Blue assay followed by Crystal Violet. Results are expressed as % of the cell growth observed with control buffer.

The following PRO polypeptides tested positive in this assay: PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 and PRO10096.

EXAMPLE 20: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes

overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from a panel of nine different tumor tissues (listed below) were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues, as compared to a non-cancerous human tissue control or other human tumor tissues. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
PRO6004	colon tumor	universal normal control
PRO4981	colon tumor	universal normal control
PRO4981	lung tumor	universal normal control
PRO7174	colon tumor	universal normal control
PRO5778	lung tumor	universal normal control
PRO5778	breast tumor	universal normal control
PRO5778	liver tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
	PRO4332	colon tumor	universal normal control
5	PRO9799	colon tumor	universal normal control
	PRO9909	colon tumor	universal normal control
10	PRO9917	colon tumor	universal normal control
	PRO9917	lung tumor	universal normal control
	PRO9917	breast tumor	universal normal control
	PRO9771	colon tumor	universal normal control
15	PRO9877	colon tumor	universal normal control
	PRO9903	colon tumor	universal normal control
	PRO9830	colon tumor	universal normal control
20	PRO7155	colon tumor	universal normal control
	PRO7155	lung tumor	universal normal control
	PRO7155	prostate tumor	universal normal control
25	PRO9862	colon tumor	universal normal control
	PRO9882	colon tumor	universal normal control
	PRO9864	colon tumor	universal normal control
30	PRO10013	colon tumor	universal normal control
	PRO9885	colon tumor	universal normal control
35	PRO9879	colon tumor	universal normal control
	PRO10111	colon tumor	universal normal control
	PRO10111	rectal tumor	universal normal control
40	PRO9925	breast tumor	universal normal control
	PRO9925	rectal tumor	universal normal control
	PRO9925	colon tumor	universal normal control
	PRO9925	lung tumor	universal normal control
45	PRO9905	colon tumor	universal normal control
	PRO10276	colon tumor	universal normal control
	PRO9898	colon tumor	universal normal control
50	PRO9904	colon tumor	universal normal control
	PRO19632	colon tumor	universal normal control
55	PRO19672	colon tumor	universal normal control

TABLE 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to normal control:</u>
5	PRO9783	colon tumor	universal normal control
	PRO9783	lung tumor	universal normal control
	PRO9783	breast tumor	universal normal control
	PRO9783	prostate tumor	universal normal control
	PRO9783	rectal tumor	universal normal control
10	PRO10112	colon tumor	universal normal control
	PRO10284	colon tumor	universal normal control
	PRO10100	colon tumor	universal normal control
15	PRO19628	colon tumor	universal normal control
	PRO19684	colon tumor	universal normal control
	PRO10274	colon tumor	universal normal control
20	PRO9907	colon tumor	universal normal control
	PRO9873	colon tumor	universal normal control
	PRO10201	colon tumor	universal normal control
25	PRO10200	colon tumor	universal normal control
	PRO10196	colon tumor	universal normal control
	PRO10282	lung tumor	universal normal control
30	PRO10282	breast tumor	universal normal control
	PRO10282	colon tumor	universal normal control
	PRO10282	rectal tumor	universal normal control
	PRO19650	colon tumor	universal normal control
35	PRO21184	lung tumor	universal normal control
	PRO21184	breast tumor	universal normal control
	PRO21184	colon tumor	universal normal control
	PRO21201	breast tumor	universal normal control
40	PRO21201	colon tumor	universal normal control
	PRO21175	breast tumor	universal normal control
	PRO21175	colon tumor	universal normal control
	PRO21175	lung tumor	universal normal control
45	PRO21340	colon tumor	universal normal control
	PRO21340	prostate tumor	universal normal control
	PRO21384	colon tumor	universal normal control
	PRO21384	lung tumor	universal normal control
50	PRO21384	breast tumor	universal normal control
	PRO21384	lung tumor	universal normal control
	PRO21384	breast tumor	universal normal control

EXAMPLE 21: Tissue Expression Distribution

Oligonucleotide probes were constructed from the PRO polypeptide-encoding nucleotide sequence shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human adult and/or fetal tissue sources and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tissues tested. Knowledge of the expression pattern or the differential expression of the PRO polypeptide-encoding nucleic acid in various different human tissue types provides a diagnostic marker useful for tissue typing, with or without other tissue-specific markers, for determining the primary tissue source of a metastatic tumor, and the like. The results of these assays demonstrated the following:

(1) the DNA94849-2960 molecule is significantly expressed in the following tissues: cartilage, testis, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen aortic endothelial cells and uterus, and not significantly expressed in the following tissues: HUVEC.

(2) the DNA100272-2969 molecule is significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen and aortic endothelial cells; and not significantly expressed in uterus. Among a panel of normal and tumor cells examined, the DNA100272-2969 was found to be expressed in normal esophagus, esophageal tumor, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

(3) the DNA108696-2966 molecule is highly expressed in prostate and also expressed in testis, bone marrow and spleen. The DNA108696-2966 molecule is expressed in normal stomach, but not expressed in stomach tumor. The DNA108696-2966 molecule is not expressed in normal kidney, kidney tumor, normal lung, or lung tumor. The DNA108696-2966 molecule is highly expressed in normal rectum, lower expression in rectal tumor. The DNA108696-2966 molecule is not expressed in normal liver or liver tumor. The DNA108696-2966 molecule is not expressed in normal esophagus, esophageal tumor, cartilage, HUVEC, colon tumor, heart, placenta, adrenal gland, aortic endothelial cells and uterus.

(4) the DNA119498-2965 molecule is significantly expressed in the following tissues: highly expressed in aortic endothelial cells, and also significantly expressed in cartilage, testis, HUVEC, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate and spleen. It is not significantly expressed in uterus.

(5) the DNA119530-2968 molecule is expressed in the following tissues: normal esophagus and not expressed in the following tissues: esophageal tumors, stomach tumors, normal stomach, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumors, normal liver or liver tumors.

(6) the DNA129794-2967 molecule is significantly expressed in testis and adrenal gland; and not significantly expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, prostate, spleen, aortic endothelial cells and uterus.

(7) the DNA131590-2962 molecule is significantly expressed in the following tissues: bone marrow, adrenal

gland, prostate, spleen, uterus, cartilage, testis, colon tumor, heart, and placenta, and not significantly expressed in the following tissues: HUVEC, and aortic endothelial cells.

(8) the DNA149995-2871 molecule is highly expressed in testis, and adrenal gland; expressed in cartilage, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, prostate and uterus; weakly expressed in bone marrow, spleen and aortic endothelial cells; and not significantly expressed in placenta.

5 (9) the DNA167678-2963 molecule is significantly expressed in the following tissues: normal esophagus, esophageal tumor, highly expressed in normal stomach, stomach tumor, highly expressed in normal kidney, kidney tumor, expressed in lung, lung tumor, normal rectum, rectal tumor, weakly expressed in normal liver, and not significantly expressed in liver tumor.

10 (10) the DNA168028-2956 molecule is highly expressed in bone marrow; expressed in testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, adrenal gland, prostate, spleen, aortic endothelial cells and uterus; and is weakly expressed in cartilage. Among a panel of normal and tumor samples examined, the DNA168028-2956 was found to be expressed in stomach tumor, normal kidney, kidney tumor, lung tumor, normal rectum and rectal tumor; and not expressed in normal esophagus, esophageal tumor, normal stomach, normal lung, normal liver and liver tumor.

15 (11) the DNA176775-2957 molecule is highly expressed in testis; expressed in cartilage and prostate; weakly expressed in adrenal gland, spleen and uterus; and not significantly expressed in human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow and aortic endothelial cells.

20 (12) the DNA177313-2982 molecule is significantly expressed in prostate and aortic endothelial cells; and not significantly expressed in cartilage, testis, human umbilical vein endothelial cells (HUVEC), colon tumor, heart, placenta, bone marrow, adrenal gland, spleen and uterus. Among a panel of normal and tumor cells, the DNA177313-2982 molecule was found to be expressed in esophageal tumor but not in normal esophagus, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure
25 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure
30 NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure
35 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25),
5 Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).
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3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence

selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figures 1A-1B (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figures 59A-59B (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), and Figure 243 (SEQ ID NO:243).

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4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.
6. A host cell comprising the vector of Claim 5.
7. The host cell of Claim 6, wherein said cell is a CHO cell.
8. The host cell of Claim 6, wherein said cell is an *E. coli*.
9. The host cell of Claim 6, wherein said cell is a yeast cell.
10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure

166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), and Figure 244 (SEQ ID NO:244).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ

ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50
 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure
 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64),
 Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID
 NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ
 5 ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88
 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure
 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102),
 Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ
 ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure
 10 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID
 NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure
 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID
 NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure
 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID
 15 NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure
 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID
 NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure
 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID
 NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure
 20 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID
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 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID
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 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID
 25 NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure
 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID
 NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or
 Figure 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2
 30 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ
 ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18
 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure
 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32),
 Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID
 35 NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ
 ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56
 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure

64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100),
 5 Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure
 10 Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure
 20 Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure
 30 Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure
 35 Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ

ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94
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 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID
 NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure
 10 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID
 NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure
 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID
 NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure
 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID
 15 NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure
 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID
 NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure
 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID
 NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure
 20 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID
 NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure
 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80% amino acid sequence identity to:
 - 25 (a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ
 ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID
 NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ
 ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28
 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure
 30 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42),
 Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID
 NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ
 ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66
 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure
 35 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80),
 Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID
 NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ

5 ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure
 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID
 NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure
 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID
 NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure
 5 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID
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 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID
 NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure
 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID
 10 NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure
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 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID
 NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure
 15 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID
 NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure
 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID
 NO:242), or Figure 244 (SEQ ID NO:244), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ
 20 ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID
 NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ
 ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26
 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure
 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40),
 25 Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID
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 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure
 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78),
 30 Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID
 NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ
 ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102
 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108),
 Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ
 35 ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure
 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID
 NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure

138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), or Figure 244 (SEQ ID NO:244), lacking its associated signal peptide.

20. A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO982, PRO1160, PRO1187, or PRO1329 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

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21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO357, PRO229, PRO1272 or PRO4405 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

25

22. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide, wherein the release of TNF- α from said blood is stimulated.

23. A method for stimulating the proliferation of normal human dermal fibroblast cells, said method comprising contacting said cells with a PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO229, PRO1272, PRO181, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO788, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1194, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1488, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO5723, PRO1801, PRO4333, PRO3543, PRO3444, PRO4302, PRO4322, PRO5725, PRO4408, PRO9940, PRO7154, PRO7425, PRO6079, PRO9836 or PRO10096 polypeptide, wherein the proliferation of said cells is stimulated.

35

24. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

5

25. The method of Claim 24, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, or liver tumor.

26. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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FIGURE 1A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTTGCTCGAACCAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
TTTTCGGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT
GTTCAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA
TTTGAAGATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCGGAAAATGATGTGTCATTCCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACT
TTGCTCCTACTATTTCAGGAAATTAAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
CTTCAATGGCCAACAAGGAATTATTATTCAAAATTTTAGCACAAAGATCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACCTTGTTGGCTGCCAACAAGCTAGGCACA
ACCAATGCGAGCCTGCCTCTTAACCTCCAAGTACAGCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCTCTTTACCAGCATATTCT
ACCTGAAGAATGCCATTCTACAATAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT
TCTACTCTTTTTGATTAGCTACATTACCTTGTTGAAGCAGTACACATTGTCCTTTTTTTAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAACTAC
AATTTTTCAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTCCCTGTTTCAAT
AAGAGTCAATCCACATTTACAAAGATGATTTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCTTCAGATTATTTCTTCAAATATAACATATCTAGATTTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTGT
AAGTTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAATAATATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCA
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA
TGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT
TTTCTTTTCACTAGTCCAAGCCAAAATTTTAAGATGATTTGTCAGAAAGGGCACAAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGTGGCAGCTAA
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATAGCCATTTTCAGTGCAAACAAGTAAAATCAAAAAGACCATCCTTTATTT
TTCCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA
AACTACATTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAG
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAACTGTGATTTTTTTCTTCAAGTAAAACCTTAGT
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT
AAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTAGAACAAATATGGCATT
TAACCTTTATTTATTTGCTTTTAAGAAATATTCTTTGTGGAATTGTTGAATAAACTATAA
AATATTATTTTGATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTACTAGAAAT

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FIGURE 1B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCCTTATGTTAGAAGAGACTTTCCTTGAGTGACATTTTTTAAATA
GAGGAGGTATTCATATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTCAGG
ANTATATTTTCTACAAGTTCACCTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAACATATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAAGTGAAGAAATTACCCAG
GTAATTCAGGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTATAACCTGATGTAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTATCAATTAAAAA

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FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSII FAGGDKWSV D P R V S I S T L N K R D Y S L Q I Q N V D V T D D G P Y T C S V Q T Q H
TPRTMQVHLTVQVPPKIYDISNDMTVN E G T N V T L T C L A T G K P E P S I S W R H I S P S A K P F E N G Q
YLDIYGITRDQAGEYECSAENDVSFPDVRKV K V V V N F A P T I Q E I K S G T V T P G R S G L I R C E G A
GVPPPAFEWYKGEKKLFNGQQGII I Q N F S T R S I L T V T N V T Q E H F G N Y T C V A A N K L G T T N A S L
PLNPPSTAQYGITGSADVL F S C W Y L V L T L S S F T S I F Y L K N A I L Q
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

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FIGURE 3

CACTGCCCCGTCCGCTCTTCAGCAGCCGGTCGCGGGCGGTGGAAAAGCGAGTGAAGAGAGCGC
GACGGCGGGCGGGCGGGCGGGCGGCAGCTATTGCTGGACGGCCAGTGGGAGAGCGAGGCCTGAG
CCTCTGCGTCTAGGATCAAAATGTTTTCAATCCCAGAATACTATGAAGGCAAGAACGTCCTC
CTCACAGGAGCTACCGGTTTTCTAGGGAAGGTGCTTCTGGAAAAGTTGCTGAGGTCTTGTCC
TAAGGTGAATTCAGTATATGTTTTGGTGAGGCAGAAAGCTGGACAGACACCACAAGAGCGAG
TGGAGAAGTCCTTAGTGGCAAGCTTTTTGACAGATTGAGAGATGAAAATCCAGATTTTAGA
GAGAAAATTATAGCAATCAACAGCGAACTCACCCAACCTAACTGGCTCTCAGTGAAGAAGA
TAAAGAGGTGATCATAGATTCTACCAATATTATATTCCACTGTGCAGCTACAGTAAGGTTTA
ATGAAAATTTAAGAGATGCTGTTTCAAGTTAAATGTGATTGCAACGCGACAGCTTATTCTCCTT
GCACAACAAATGAAGAATCTGGAAGTGTTTCATGCATGTATCAACAGCATATGCCACTGTAA
TCGCAAGCATATTGATGAAGTAGTCTATCCACCACCTGTGGATCCCAAGAAGCTGATTGATTCT
TTAGAGTGGATGGATGATGGCCTAGTAAATGATATCACGCCAAAATTGATAGGAGACAGACC
TAATACATACATATACACAAAAGCATTGGCAGAAATATGTTGTACAACAAGAGGAGCAAAAC
TAAATGTGGCAATTGTAAGGCCATCGATTGTTGGTGCCAGTTGGAAAGAACCTTTTCCAGGA
TGGATTGATAACTTTAATGGACCAAGTGGTCTCTTTATTGCGGCAGGGAAAGGAATTCCTCG
AACATACGTGCCTCCAACAATGCCCTTGACAGATCTTGTTCTGTAGATGTAGTTGTCAACA
TGAGTCTTGCGGCAGCCTGGTATTCCGGAGTTAATAGACCAAGAAACATCATGGTGTATAAT
TGTACAACAGGCAGCACTAATCCTTTCCACTGGGGTGAAGTTGAGTACCATGTAATTTCCAC
TTTCAAGAGGAATCCTCTCGAACAGGCCTTCAGACGGCCCAATGTAAATCTAACCTCCAATC
ATCTTTTATATCATTACTGGATTGCTGTAAGCCATAAGGCCCCAGCATTCTGTATGATATC
TACCTCAGGATGACTGGAAGAAGCCCAAGGATGATGAAAACAATAACTCGTCTTCACAAAGC
TATGGTGTCTTGAATATTTACAAGTAATTTCTGGGTTTGAATACTGAGAATGTCAATA
TGTTAATGAATCAACTAAACCCTGAAGATAAAAAGACCTTCAATATTGATGTACGGCAGTTA
CATTGGGCAGAAATATATAGAGAACTACTGCTTGGAACCTAAGAAGTACGTATTGAAGTAAGA
AATGTCTGGCCTCCCTGCAGCCAGAAAACATCTGAACAAGTTGCGGAATATACGTTATGGTT
TTAATACTATCCTTGTGATCCTCATCTGGCGCATTTTTATTGCAAGATCACAAATGGCAAGA
AATATCTGGTACTTTGTGGTTAGTCTGTGTTACAAGTTTTTGTCTACTTCCGAGCATCCAG
CACTATGAGATACTGAAGACCAAGGATTCAGCATTAGAACATCTATACATATGGTGATCTAA
ATGTACAAAATGTAAAATGTATAAGTCATCTCACTTTTTGTCAAGACATTAAACCATCTTAG
ATCGGAGTGTGAAGTAAATTATGGTATATTTTATGTAACATTTTAATGTTTATGCTCATAAA
ACTTAGTGAACACACTGTGTTATGCCAGCTCAAATCTACAGTAGCCACCAAAACCATGACTT
AATATTTTGAAGCCCTAGAAGAAAGGGTGTGCTGAGGACAAGAGTGGGGAAATAGGAACACT
GACCAGTATAACTGTGCAATTCTGGAACATATTAATTAATAATATGCCTTAACATATAGT
GAATTTCTAATTCTAATGTTTCAAGTGCAATGGAAGACATTTATTTGGACAGTATACTAGCAAA
GTTGGTAGATATTTGATTCTTCATTTTTTGTTTTTTTCATTAGTTGAAGTGGGTTTTAGTTT
TGTTTAAAATTATAACCAGCGTATTTTACATCATTCTGTAAGTTAAATGATATCAACATG
AAAGAGATGTTCTCATTTTTCTTTTTCTGATTAAACGTCTGATGCATATCATTTTTCTATAA
GTAATCAGTTGCTTTTAAAATCAGAAGGCTATATTATTCTAATGACCCTATTGATCTAAAT
GGGTTTGAGAATCCATATCAGCAACATACGTGTTTTTGGACAGAAAGTGAACAAATTCGG
TAAACTGTTAGTATCAAAAAGAATAGGAATACAGTTTTCTTTTCCACATTATGATCAATAAA
AATCTTGTGAGATTGTTAAAAA

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FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA94849
><subunit 1 of 1, 515 aa, 1 stop
><MW: 59357, pI: 9.40, NX(S/T): 3
MVSIP EYYEGKNVLLTGATGFLGKVLLEKLLRSCPKVNSVYVLVRQKAGQTPQERVEEVL
SGKLFDRRLDENPDFREKIIAINSELTQPKLALSEEDKEVIIDSTNIIIFHCAATVRFNEN
LRDAVQLNVIATRQLILLAQQMKNLEVFMHVSTAYAYCNRKHIDEVVYPPPVDPKKLIDS
LEWMDDGLVNDITPKLIGDRPNTYIYTKALAEYVVQQEGAKLNVAIVRPSIVGASWKEPF
PGWIDNFNGPSGLFIAAGKGILRTIRASNNALADLVPVDVVVNMSLAAAWYSGVNRPRNI
MVYNCTTGSTNPFHWGEVEYHVISTFKRNPLEQAFRRPNVNLT SNHLLYHYWIAVSHKAP
AFLYDIYLRMTGRSPRMMKTITRLHKAMVFLEYFTSNVWNTENVNMLMNQLNPEDKKT
FNIDVRQLHWA EYIENYCLGTKKYVLNEEMSGLPAARKHLNKLNRNIRYGFNTILVILIWR
IFIARSQMARNIWIYFVVSLCYKFLSYFRASSTMRY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 469-488

N-glycosylation sites:

Amino acids 283-287;304-308;341-345

Tyrosine kinase phosphorylation site:

Amino acids 160-169

N-myristoylation sites:

Amino acids 219-225;252-258;260-266;452-458

Leucine zipper pattern:

Amino acids 439-461

FIGURE 5

[illegible]

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FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96883
><subunit 1 of 1, 514 aa, 1 stop
><MW: 55687, pI: 8.78, NX(S/T): 2
MPAVSGPGPLFCLLLLLLDPHSPETGCPPLRRFEYKLSFKGPRLALPGAGIPFWSHHGDA
ILGLEEVRLTPSMRNRSGAVWSRASVPFSAWEVEVQMRVTGLGRRGAQGMVWYTRGRGH
VGSVLGGLASWDGIGIFFDSPAEDTQDSPAIRVLASDGHIPSEQPGDGASQGLGSCHWDF
RNRPHSFRARITYWGQRLRMSLNSGLTPSDPGEFCVDVGPLLLVPGGFFGVSAATGTLAG
EDPTGQVPPQPFFLEMQQLRLARQLEGLWARLGLGTREDVTPKSDSEAQGEGERLFDLEET
LGRHRRILQALRGLSKQLAQAEQWKKQLGPPGQARPDGGWALDASCQIPSTPGRGGHLS
MSLNKDSAKVGAALLHGQWTLQALQEMRDAAVRMAAEAQVSYLPVGIEHHFLELDHILGL
LQEELRGPAKAAAKAPRPPGQPPRASSCLQPGIFLFYLLIQTVGFFGYVHFRQELNKSLO
ECLSTGSLPLGPAPHTPRALGILRRQPLPAMPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 215-232;450-465

N-glycosylation sites:

Amino acids 75-79;476-480

Glycosaminoglycan attachment site:

Amino acids 5-9

N-myristoylation sites:Amino acids 78-84;122-128;126-132;168-174;172-178;
205-211;226-232;230-236;236-242;356-362**Amidation site:**

Amino acids 102-106

FIGURE 7

[illegible]

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FIGURE 8

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96894
><subunit 1 of 1, 361 aa, 1 stop
><MW: 40747, pI: 9.20, NX(S/T): 1
MAWQGWPAAWQWVAGCWLLLVLLVLLVSPRGCRARRGLRGLLMAHSQRLFRIGYSLYT
RTWLGYLEFYRQQLRRARNRYPKGHSKTQPRLFNGVKVLPPIVLSDNYSYLIIDTQAQLAV
AVDPSDPRAVQASIEKEGVTLVAILCTHKKHWDHSGGNRDLRRHRDCRVYGSPQDGIPYL
THPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPIYKGPSCLFSGDLLFLSGCGRTF
EGNAETMLSSLDTVLGLGDDTLLWPGHEYAEENLGFAGVVEPENLARERKMQWVQRQRLE
RKGTCPSTLGEERSYNPFLRTHCLALQEALGPGPGPTGDDDDYSRAQLLEELRRLKDMHKS
K
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

N-glycosylation site:

Amino acids 106-110

Glycosaminoglycan attachment site:

Amino acids 234-238

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 301-305

Tyrosine kinase phosphorylation site:

Amino acids 162-171

N-myristoylation sites:

Amino acids 41-47;235-241;242-248;303-309

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 6-17

cAMP phosphodiesterases class-II proteins:

Amino acids 144-161

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FIGURE 9

GCTGACAATCCCCTTGACGTTCTATCCCGGAAGCTCCACCTGGGGCCCAATGTTGGGCGTGA
TGTTCCCTCGCCTGTCTCTGCCTGGAAACTGGTCTTCCCAAGCTCCACTGGCAGCCACTTCT
CCATGTTGGGCATCGGAGACATCGTTATGCCTGGTCTCCTACTATGCTTTGTCCTTCGCTAT
GACAACTACAAAAAGCAAGCCAGTGGGGACTCCTGTGGGGCCCCTGGACCTGCCAACATCTC
CGGGCGCATGCAGAAGGTCTCCTACTCTCACTGCACCCTCATCGGATACTTTGTAGGCCTGC
TCACTGCTACTGTGGCGTCTCGCATTACCGGGCCGCCAGCCCGCCCTTCTCTATTTGGTG
CCATTTACTTTATTGCCACTCCTCACGATGGCCTATTTAAAGGGCGACCTCCGGCGGATGTG
GTCTGAGCCTTTCCACTCCAAGTCCAGCAGCTCCCGATTCTGGAAGTATGATGGATCACGT
GGAAAGTGACCAGATGGCCGTCATAGTCCTTTTCTCTCAACTCATGGTTTGTTTCCTCTTAG
AGCTGGCCTGGTACTCAGAAATGTACCTGTGTTTAAGGAACTGCCGTGTGACTGGATTGGC
ATTGAAAGGGAGCTCGTTTGCAGGAGAGAGGTGCTGGAGCCCTGTTTGTTTCCTTCTCTTCC
TGCGGATGTAGAGGTGGGGCCCCTTCCAAGAGGGACAGGCCTCTCCCAGCGCGCCTTCCTC
CCACGTTTTTATGGATCTGCACCAGACTGTTACCTTCTGGGGGAGATGGAGATTGACTGTT
TAAAAACTGAAAACAGCGAGGAGTCTTTCTAGAACTTTTGAACACTAAAAGGATGAAAAAT
TAGC

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FIGURE 10

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA100272
><subunit 1 of 1, 108 aa, 1 stop
><MW: 12055, pI: 4.69, NX(S/T): 0
MMDHVESDQMAVIVLFSQLMVCFLLELAWYSEMYLCLRNCRVTGFGIERELVCRREVLEP
CLVPSLPADVEVGPLPRGTGLSPARLPPTFLWICTRLLPSGGDGLTV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-myristoylation site:

Amino acids 80-86

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FIGURE 11

TCGCACACTGGTGGCTTCAGAAGAAATTCTCAACACCTAGCTCGCCAGAGAGTCTATGTATG
GGATTGAACAATCTGTAAACTAAAGGATCCTAATCATGAAAATAAGTATGATAAATTATAAG
TCACTATTGGCACTGTTGTTTATATTAGCCTCCTGGATCATTTTTACAGTTTTCCAGAACTC
CACAAAGGTTTGGTCTGCTCTAAACTTATCCATCTCCCTCCATTACTGGAACAACTCCACAA
AGTCCTTATTCCCTAAAACACCACTGATATCATTAAGCCACTAACAGAGACTGAACTCAGA
ATAAAGGAAATCATAGAGAACTAGATCAGCAGATCCCACCCAGACCTTCACCCACGTGAA
CACCACCACCAGCGCCACACATAGCACAGCCACCATCCTCAACCCTCGAGATACGTACTGCA
GGGAGACCAGCTGCACATCCTGCTGGAGGTGAGGGACCACTTGGGACGCAGGAAGCAATAT
GGCGGGGATTTCTGAGGGCCAGGATGTCTTCCCCAGCGCTGATGGCAGGTGCTTCAGGAAA
GGTGACTGACTTCAACAACGGCACCTACCTGGTCAGCTTCACTCTGTTCTGGGAGGGCCAGG
TCTCTCTGTCTGCTGCTCATCCACCCAGTGAAGGGGTGTCAGCTCTCTGGAGTGAAGG
AACCAAGGCTATGACAGGGTGATCTTCACTGGCCAGTTTGTCAATGGCACTTCCCAAGTCCA
CTCTGAATGTGGCCTGATCCTAAACACAAATGCTGAATTGTGCCAGTACCTGGACAACAGAG
ACCAAGAAGGCTTCTACTGTGTGAGGCCTCAACACATGCCCTGTGCTGCACTCACTCACATG
TATTCTAAGAACAAGAAAGTTTCTTATCTTAGCAAACAAGAAAAGAGCCTCTTTGAAAGGTC
AAATGTGGGTGTAGAGATTATGGAAAAATTCAATACAATTAGTGTCTCCAAATGCAACAAAG
AAACAGTTGCAATGAAAGAGAAATGCAAGTTTGGGAATGACATCCACAATCCCCAGTGGGCAT
GTCTGGAGAAACACATGGAATCCTGTCTCCTGTAGTTTGGCTACAGTCAAATGAAGGAATGC
CTGAGAGGAAAACATATACCTAATGGGAGATTCCACGATCCGCCAGTGGATGGAATACTT
CAAAGCCAGTATCAACACACTGAAGTCAGTGGATCTGCATGAATCTGGAAAATTGCAACACC
AGCTTGCTGTGGATTTGGATAGGAACATCAACATCCAGTGGCAAAAATATTGTTATCCCTTG
ATAGGATCAATGACCTATTCAGTCAAAGAGATGGAGTACCTCACCCGGGCCATTGACAGAAC
TGGAGGAGAAAAAATACTGTCATTGTTATTTCCCTGGGCCAGCATTTTCAGACCCTTTCCCA
TTGATGTTTTTATCCGAAGGGCCCTCAATGTCCACAAAGCCATTTCAGCATCTTCTTCTGAGA
AGCCCAGACACTATGGTTATCATCAAAACAGAAAACATCAGGGAGATGTACAATGATGCAGA
AAGATTTAGTGACTTTTCATGGTTACATTCAATATCTCATCATAAAGGACATTTTCCAGGATC
TCAGTGTGAGTATCATTGATGCCTGGGATATAACAATTGCATATGGCACAAATAATGTACAC
CCACCTCAACATGTAGTCGGAAATCAGATTAATATATTATTAACTATATTTGTAAATAACAA

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FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108696
><subunit 1 of 1, 544 aa, 1 stop
><MW: 62263, pI: 9.17, NX(S/T): 7
MKISMINYKSLALLFILASWIIFTVFQNSTKVWSALNLSISLHYWNNSTKSLFPKTPLI
SLKPLTETELRIKEIIEKLDQQIPPRPFTHVNTTTSATHSTATILNPRDTYCRGDQLHIL
LEVRDHLGRRKQYGGDFLRARMSSPALMAGASGKVTDFFNNGTYLVSFTLFWEGQVSLSL
LIHPSEGVSALWSARNQGYDRVIFTGQFVNGTSQVHSECGLILNTNAELCOYLDNRDQEG
FYCVRPQHMPCAALTHMYSKNKKVSYLSKQEKSLFERSNVGVEIMEKFNTISVSKCNKET
VAMKEKCKFGMTSTIPSGHVWRNTWNPVSCSLATVKMKECLRGKLIYLMGDSTIRQWMEY
FKASINTLKSVDLHESGKLQHQLAVDLDRNINIQWQKYCYPLIGSMTYSVKEMEYLTRAI
DRTGGEKNTVIVISLGQHFRRFPIDVFIRRALNVHKAIQHLLLRSPDTMVIKTNIREM
YNDAERFSDFHGYIQYLIKIDIFQDLSVSIIDAWDITIAYGTNNVHPPQHVVGNQINILL
NYIC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 29-33;38-42;47-51;48-52;92-96;160-164;210-214

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 262-266

Tyrosine kinase phosphorylation site:

Amino acids 236-243;486-494

N-myristoylation sites:

Amino acids 206-212;220-226;310-316;424-430;533-539

Amidation site:

Amino acids 127-131

Cell attachment sequence:

Amino acids 113-116

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FIGURE 13

GCAAAGAGAAGACTGAAAAGACAAACCTGGGTGCAGCCAGAGAGGTCCAGATAGATGAGCTTG
TGGCATCCATTCCCCAAGTTCAGCCTAGGGACTCCACGTACCCCAGCTGGGTCTCATTGTTC
CAGAACTGCATTAGTTAAGATTACCCAGACTTGGATTTCAAAGGAATACTTTTCATTGTTCCG
TCTGTAACACGAAGTAATTGGGGCCAGCTGGATGTCAGG**ATG**CGTGTGGTTACCATTGTAAT
CTTGCTCTGCTTTTGTCAAAGCGGCTGAGCTGCGCAAAGCAAGCCCAGGCAGTGTGAGAAAGCC
GAGTGAATCATGGCCGGGCGGGTGGAGGCCGGAGAGGCTCCAACCCGGTCAAACGCTACGCA
CCAGGCCTCCCGTGTGACGTGTACACATATCTCCATGAGAAATACTTAGATTGTCAAGAAAG
AAAATTAGTTTATGTGCTGCCTGGTTGGCCTCAGGATTTGCTGCACATGCTGCTAGCAAGAA
ACAAGATCCGCACATTGAAGAACAACATGTTTTCCAAGTTTAAAAAGCTGAAAAGCCTGGAT
CTGCAGCAGAATGAGATCTCTAAAATTGAGAGTGAGGCGTTCTTTGGTTTAAACAACTCAC
CACCTCTTACTGCAGCACAAACCAGATCAAAGTCTTGACGGAGGAAGTGTTCATTTACACAC
CTCTCTTGAGCTACCTGCGTCTTTATGACAACCCCTGGCACTGTACTTGTGAGATAGAAACG
CTTATTTCAATGTTGCAGATTCCCAGGAACCGGAATTTGGGGAACTACGCCAAGTGTGAAAG
TCCACAAGAACAAAAAAATAAAAACTGCGGCAGATAAAATCTGAACAGTTGTGTAATGAAG
AAAAGGAACAATTGGACCCGAAACCCCAAGTGTGAGGGAGACCCCCAGTCATCAAGCCTGAG
GTGGACTCAACTTTTTGCCACAATTATGTGTTTCCCATACAAACACTGGACTGCAAAAGGAA
AGAGTTGAAAAAAGTGCCAAACAACATCCCTCCAGATATTGTTAAACTTGACTTGTGCATACA
ATAAAATCAACCAACTTCGACCCAAGGAATTTGAAGATGTTTCATGAGCTGAAGAAATTAAAC
CTCAGCAGCAATGGCATTGAATTCATCGATCCTGCCGCTTTTTTAGGGCTCACACATTTAGA
AGAATTAGATTTATCAAACAACAGTCTGCAAACTTTGACTATGGCGTATTAGAAGACTTGT
ATTTTTTTGAACTCTTGTGGCTCAGAGATAACCCTTGGAGATGTGACTACAACATTCACTAC
CTCTACTACTGGTTAAAGCACCCTACAATGTCCATTTTAATGGCCTGGAATGCAAAACGCCT
GAAGAATACAAAGGATGGTCTGTGGGAAAATATATTAGAAGTTACTATGAAGAATGCCCAA
AGACAAGTTACCAGCATATCCTGAGTCATTTGACCAAGACACAGAAGATGATGAATGGGAAA
AAAAACATAGAGATCACACCGCAAAGAAGCAAAGCGTAATAATTACTATAGTAGGAT**TA**AGGT
AGAAATTGTTCTGATTGTAATTAGTTTTGTATTTTCTATACTGGTGTAGAAAACATATGTT
TACATTTGATTAACTGTGTTGCCTATTTATGCAGGGTAATCCAGCTAAAGGAAGCTTTCTTT
AATTATAAGTATTATTGTGACTATTATAGTAATCAAGAGAATGCTATCATCCTGCTTGCCTG
TCCATTTGTGGAACAGCATCTGGTGATATGCAATTCACACTGGTAACCTGCAGCAGTTGGG
TCCTAATGATGGCATTAGACTTTTCATAATGTCCTGTATAAATGTTTTTACTGCTTTTAGAAA
ATAAAGAAAAAAACTTGGTTCATGTTTAAAA

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FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA117935
><subunit 1 of 1, 440 aa, 1 stop
><MW: 51670, pI: 8.70, NX(S/T): 2
MRVVTIVILLCFCKAAELRKASPGSVRSRVNHGRAGGRRGSNPVKRYAPGLPCDVYTYL
HEKYLDQCERKLVYVLPGWPDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQQNEISKI
ESEAFFGLNKLTTLLLOHNQIKVLTEEVFIYTPLLSYLRLYDNPPWHCTCEIETLISMLQI
PRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVIKPEVDSTF
CHNYVFPIQTLDCRKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFEDVHELKKLNLSS
NGIEFIDPAAFLGLTHLEELDLSNNSLQNFQVLEEDLYFLKLLWLRDNPWRCDYNIHYL
YYWLKHHYNVHFNGLECKTPEEYKGWSVGKYIRSYYEECPKDKLPAYPESFDQDTEDEW
EKKHRDHTAKKQSVIITIVG
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 297-301;324-328

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 19-23;39-43;430-434

N-myristoylation sites:

Amino acids 24-30;37-43

Amidation site:

Amino acids 37-41

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FIGURE 15

GCGGCAGCAGCGCGGGCCCCAGCAGCCTCGGCAGCCACAGCCGCTGCAGCCGGGGCAGCCTC
CGCTGCTGTGCGCTCCTCTGATGCGCTTGCCCTCTCCCGGCCCCGGGACTCCGGGAGA**ATGT**
GGGTCCTAGGCATCGCGGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTGCGCTGCAA
ATCCAGTGCTACCAAGTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCCCGAGTTCAT
TGTGAATTGCACGGTGAACGTCAAGACATGTGTCAGAAAGAAGTGATGGAGCAAAGTGCCG
GGATCATGTACCGCAAGTCCTGTGCATCATCAGCGGCCTGTCTCATCGCCTCTGCCGGGTAC
CAGTCCTTCTGCTCCCCAGGGAACTGAACTCAGTTTGCATCAGCTGCTGCAACACCCCTCT
TTGTAACGGGCCAAGGCCCAAGAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGCCAGGGCTCC
GCACCACCATCCTGTTTCCTCAAATTAGCCCTCTTCTCGGCACACTGCT**TGA**AGCTGAAGGAGA
TGCCACCCCTCCTGCATTGTTCTTCCAGCCCTCGCCCCCAACCCCCACCTCCCTGAGTGA
GTTTCTTCTGGGTGTCCTTTTATTCTGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTGTTC
TGTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAATAAATTCAGCCTGACTGAATTTTC
AGTATGTACTTGAAGGAAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAACCGGAGT
CAAGGCCAGGCTGGCAGAGTCAGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTAA
AGCCTCCAGTGTCCATTCCATCCCTGATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGA
CCTTTTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAACCTT
CATGCTCCTGAAAACCATTTCTCTGCAGCAGAATTGGCTGGTTTCGCGCCTGAGTTGGGCTCT
ACTGACTCGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCCTCGCTCTGAAAAGTGCT
TAAGAAAATCTTCTCAGTTCTCCTTGAGAGGACTGGCGCCGGGACGCGAAGAGCAACGGGC
GCTGCACAAAGCGGGCGCTGTGCGTGGTGGAGTGCGCATGTACGCGCAGGCGCTTCTCGTGG
TTGGCGTGCTGCAGCGACAGGCGGCAGCACAGCACCTGCACGAACACCCGCCGAACTGCTG
CGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGA
AGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTGCTTGGGTTTGGCC
GCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAG
CCCTGGGCAGACACGAGCAGGAGGGAGAGACAGAGA

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FIGURE 16

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119474
><subunit 1 of 2, 141 aa, 1 stop
><MW: 15240, pI: 8.47, NX(S/T): 1
MWVLGIAATFCGLFLLPGFALQIQCYQCEEFQLNNDCCSSPEFIVNCTVNVQDMCQKEVME
QSAGIMYRKSCASSAACLIASAGYQSFCSPGKLNSVCISCCNTPLCNGPRPKKRGSSASA
LRPGLRTTILFLKLALFSAHC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 45-49

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 113-117

N-myristoylation sites:

Amino acids 5-11;115-121;124-130

Ly-6 / u-PAR domain proteins:

Amino acids 94-107

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FIGURE 17

CGCAAAGCCGCCCTCGGGGCGCTC**ATG**GGCGGGACGCCTCCTGGGAAAGGCTTTAGCCGCGGT
GTCTCTCTCTCTGGCCTTGGCCTCTGTGACTATCAGGTCCTCGCGCTGCCGCGGCATCCAGG
CGTTCAGAACTCGTTTTTCATCTTCTTGGTTTTTCATCTTAATACCAACGTCATGTCTGGTTCT
AATGGTTCCAAAGAAAATTCTCACAATAAGGCTCGGACGTCTCCTTACCCAGGTTCAAAAGT
TGAACGAAGCCAGGTTCTAATGAGAAAGTGGGCTGGCTTGTTGAGTGGCAAGACTATAAGC
CTGTGGAATACACTGCAGTCTCTGTCTTGGCTGGACCCAGGTGGGCAGATCCTCAGATCAGT
GAAAGTAATTTTTCTCCCAAGTTTAACGAAAAGGATGGGCATGTTGAGAGAAAGAGCAAGAA
TGGCCTGTATGAGATTGAAAATGGAAGACCGAGAAATCCTGCAGGACGGACTGGACTGGTGG
GCCGGGGGCTTTTGGGGCGATGGGGCCCAAATCACGCTGCAGATCCCATTTATAACCAGATGG
AAAAGGGATAGCAGTGGAAATAAAATCATGCATCCTGTTTCTGGGAAGCATATCTTACAATT
TGTTGCAATAAAAAGGAAAGACTGTGGAGAATGGGCAATCCCAGGGGGGATGTTGGATCCAGGA
GAGAAGATTAGTGCCACACTGAAAAGAGAATTTGGTGAGGAAGCTCTCAACTCCTTACAGAA
AACCAGTGCTGAGAAGAGAGAAATAGAGGAAAAGTTGCACAAACTCTTCAGCCAAGACCACC
TAGTGATATATAAGGGATATGTTGATGATCCTCGAAACACTGATAATGCATGGATGGAGACA
GAAGCTGTGAACCTACCATGACGAAACAGGTGAGATAATGGATAATCTTATGCTAGAAGCTGG
AGATGATGCTGGAAAAGTGAAATGGGTGGACATCAATGATAAACTGAAGCTTTATGCCAGTC
ACTCTCAATTCATCAAACCTTGTGGCTGAGAAACGAGATGCACACTGGAGCGAGGACTCTGAA
GCTGACTGCCATGCGTTG**TAG**CTGATGGTCTCCGTGTAAGCCAAAGGCCACAGAGGAGCAT
ATACTGAAAAGAAGGCAGTATCACAGAATTTATACTATAAAAAGGGCAGGGTAGGCCACTTG
GCCTATTTACTTTCAAAACAATTTGCATTTAGAGTGTTTCGCATCAGAATAACATGAGTAAG
ATGAACTGGAACACAAAATTTTCAGCTCTTTGGTCAAAAGGAATATAAGTAATCATATTTTG
TATGTATTTCGATTTAAGCATGGCTTAAATTAAATTTAAACAATAATGCTCTTTGAAGAATC
ATAATCAGAATAAAGATAAATTCTTGATCAGCTATA

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FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119498
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39125, pI: 8.53, NX(S/T): 2
MAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAFRNSFSSSWFHLNTNVMSGSNNGSKEN
SHNKARTSPYPGSKVERSQVPNEKVGWLVWQDYKPVEYTAVSVLAGPRWADPQISESNF
SPKFNEKDGHVERKSKNGLYEIEGRPRNPAGRTGLVGRGLLGRWGNHAAADPIITRWKR
DSSGNKIMHPVSGKHILQFVAIKRKDCGEWAI PGGMVDPGEKISATLKREFGEEALNSLQ
KTSAEKREIEEKLHKLFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
EAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRAHWSSEDSEADCHAL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation site:

Amino acids 55-59

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 179-183

N-myristoylation sites:

Amino acids 53-59;56-62

mutT domain signature:

Amino acids 215-235

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FIGURE 19

CGAGGGCTCCTGCTGGTACTGTGTTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAG
GCCATGCAGCCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCATGGGGAGCTCCAGACTGG
CAGCCCTGCTCCTGCCTCTCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGC
TTTCGCCACCTGCCCCACTGGAACACCCGCTGTCTCTGGCCTCCACACGGATGACAGTTT
CACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTGGTGGGCCCTCTTCTCCACAAAGCCTT
GGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGCTGTCAGGTGGCTCA
GGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAAGTCTTCCACATTCAA
GTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTCACC
TGTCTGAGAAGAGCCATCACATTTCCATCCCTCCCCAGACATCTCCACAAGGGACTTCGC
TCTAAAAGGACCCAACCTTCGGATCCAGAGACATGGGAAAGTCTTCCAGATTGGACTCACA
AAGGCATGGAGGACCCGAGTTCTCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTTCGGGTGA
CCATATCTTCAGGCCCTGAGGTACGCGTCTTTGTCTGCTGAGGCCACACTGTAGAGCTGCC
GAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTGGGGGCCACACTGTAGAGCTGCC
TTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAAGAGGACACTGTGA
GGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAAGTCA
GTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCC
ACTGAAGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATAACCCTTTGCAAAGACCTCC
CGAATGCCACGGCTCGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCC
CAGCTCTGCTTCAAGTTCTCTTTTGGAACAGCAGCCATGTTGAATGCCCCCACCAGACTGG
GTCTCTCACATCCTGGAATGTAAGCATGGATAACCAAGCCCAGCAGCTGATTCTTCACTTCT
CCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTCCCAGGCTTGGGGCAGGACACT
TTGGTGGCCCCCGTGTACACTGTCAGCCAGGCCCGGGGCTCAAGCCCAGTGTCACTAGACCT
CATCATTCCCTTCCCTGAGGCCAGGGTGTGTGCTGCTGGTGTGGCGGTGAGATGTCCAGTTTG
CCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCA
CTGCTGGCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTC
AGGCCCGGGCCCAGCGCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGGC
GCCTGGTGGGAGCGCTGGCTGAACTGCTACGGGCAGCGCTGGGCGGCGGGCGCGACGTGATC
GTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGTGGGCCCCGCTGCCGTGGCTCTGGGCGGC
GCGGACGCGCGTAGCGCGGGAGCAGGGCACTGTGCTGCTGCTGTGGAGCGGCGCCGACCTTC
GCCCCGTCAGCGGCCCCGACCCCCGCGCCGCGCCCCCTGCTCGCCCTGCTCCACGCTGCCCCG
CGCCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGG
ACGCGCGGCCTTTCGCAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCAGCGCAGGCAG
AGCCGCCTAGAGCTGTGCAGCCGGCTTGAACGAGAGGCCGCCCCGACTTGCAGACCTAGGTTG
AGCAGAGCTCCACCGCAGTCCCGGGTGTCT

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FIGURE 20

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119502
><subunit 1 of 1, 667 aa, 1 stop
><MW: 74810, pI: 9.55, NX(S/T): 3
MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFTGSSAYIPCRTW
WALFSTKPCVVRVWHCSRCLCQHLLSGGSGLQRLFHLLVQKSKKSSTFKFYRRHKMPAP
AQRKLLPRRHLSEKSHHISIPSPDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFS
FDLLPEARAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLP
CLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQHTQMVMAITLRCPLKLE
AALCQRHDWHTLCKDLPNATARES DGWYVLEKVDLHPQLCFKFSFGNSSHVECPHQTGSL
TSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDL
IIPFLRPGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLLTLGVLALTCLRRP
QSGPGPARPVLLHAADSEAQRRLVGALAE LLRAALGGGRDVIIDLWEGRHVARVGPLEW
LWAARTVAREQGTVLLWLGADLRPVSGPDPRAPLLALLHAAPRPLLLLAYFSRLCAK
GDIPPLRALPRYRLRLRDLRLLRALDARPF AEATSWGRLGARQRRQSRLELC SRLEREA
ARLADLG
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 455-472

N-glycosylation sites:

Amino acids 318-322; 347-351; 364-368

Glycosaminoglycan attachment site:

Amino acids 482-486

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 104-108; 645-649

Tyrosine kinase phosphorylation site:

Amino acids 322-329

N-myristoylation sites:

Amino acids 90-96; 358-364; 470-476

Eukaryotic cobalamin-binding proteins:

Amino acids 453-462

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FIGURE 21

CGGCTCGAGGCCCTTTGTGAGGGCTGTGAGCTGCGCCTGACGGTGGCACC**ATG**AGCAGCTCA
GGTGGGGCGCCCCGGGGCGTCCGCCAGCTCTGCGCCGCCCGCGCAGGAAGAGGGGCATGACGTG
GTGGTACCGCTGGCTGTGTGCGCCTGTCTGGGGTGCTGGGGGCAGTCTCTTGCGCGATCTCTG
GCCTCTTCAACTGCATCACCATCCACCCTCTGAACATCGCGGCCGGCGTGTGGATGATCATG
AATGCCCTTCATCTTGTGTGTGAGGCGCCCTTCTGCTGCCAGTTTCATCGAGTTTGCAAA
CACAGTGGCGGAGAAGGTGGACCGGCTGCGCTCCTGGCAGAAGGCTGTCTTCTACTGCGGGA
TGGCGGTTCGTTCATCGTCATCAGCCTGACCCTGACCACGCTGCTGGGCAACGCCATCGCC
TTTGCTACGGGGGTGCTGTACGGACTCTCTGCTCTGGGCAAAAAGGGCGATGCGATCTCCTA
TGCCAGGATCCAGCAGCAGAGGCAGCAGGCGGATGAGGAGAAGCTCGCGGAGACCCTGGAGG
GGGAGCTGT**TGA**AGGGCTGGGCGCCCTCCCTCCCTGTCCCTCTTCTGGCTCTGTGTGGGTC
CAAGTGAGGCCTGGACTGTCCACGCTGAGGCACAGCCTGGAGAGGGGCCTTTGCACGTGTCC
CTACACCTGGAGTCTCTGCTCCTTTCTCCAGACTGGCTTAAGCCAGGAGCCACTGGCTGCT
GGTGTGAGGGTCTGGGCTGCTGGACTTGAGGCAGAGCCTGCAGCAGCTGTGTGGACACTACC
CAGCCCTACTCCTCTGCTGGGTGGGTCTGCAGATCTCACACCACAGACAGGGCTGCCTGTGA
CCTGCTGTGACCTGGGAGCAGCTTCCCTGGAGATGCTGGTCTTGAGGGGAGGGGCA
AGTGGGACCCCTGCCACCTGGGCACTGAGCAGAGGGACCTCCCCAGCTCTCTTAGCAGGTGG
AGCCCCAGGGCCTGGGACAGCCTGCCGCTGCCAGCAACCTCCCACTGCTGCCTAGGGTGCAG
CGCCCACTGTACCCCTGCCTTCTGAAGAAGCCCCACAGGGCTCCTAAGGTGCACCCCGGTACC
TGGAAGTGCAGCCTTGCGAGTGACTGGACAGCTGGGTGGGGATGCTCCCTGCTGGCCCTGG
GAACCTTGACAGGCCACCTCAAGGCCCTCGGCTGCCCTCCTCCCTGGGCCTGCTGGGGC
CCCTAGGTTCTACCCATCACCCCCCGCCCTGCTGGCCTTGGTGCTAAGGAAGTGGGGAGAG
CAGGCTCTCCCTGGCACCGAGGGTGCCACCCCTCTCCCTGGTGTGGCCCCGTCAACATCAGC
CACAGCCCAGCCCCATTAGTGGGTAGTGGGTCTGACCTCAGCCCCACTCAGGTGCTCCTGC
TGGCCTGCCCAAGCCCTGCCCTCAGGGAGCTTCTGCCTTTTAAGAACTGGGCAGAGGCCACAGT
CACCTCCCCACACAGAGCTGTCCCCACTGCCCTGGGTGCCAGGCTGTCCGGAGCCAGGCCTA
CCCAGGGAGGATGCAGAGAGCTGGTGCCAGGATGTGCACCCCCATATTCCTCTGCCCTGT
GGCCTCAGCCCGCTGGCCTCTCTGACCGTGAGGCTGGCTCTCAGCCATCGGGCAGGTGCCTG
GTCAGGCCTGGCTTAGCCCAGGTGGGGCTTGGCAGAAGCGGGCGGGTGTGGAAGATATTCCA
TCTGGGGCCAACCCCAGGCTGGGCCTGCGCTGAGCTTCTGGAGCGCAGGTACTGGGTCTTGC
TAAGTGAAGTGTTCAGGAACACCTCTCGGGCCATCTGCGTCTGAGGCTGGGAGTGGCA
TCTGAGGCCGGGAGTGGCATCTGAGGCCAGGAGTGGCAGGCTGGTGGGCTGGGCGTGGGGTT
TTCTGGGCCCTGCCAGTACTGCCCTGGGGACTTGGTGGGCTCCTGGGTGAGCAGCATCCCA
CCCCTGGGAGTCTGGCCAGCTGAGCCCCAGGGTGGCAGGGGCATTATAGCCTGGTGGACATG
TGCCTTCAGGGTTCTCCGGGGCCACCTTCCTCAGGCCAGTGCTGGGTTCAAAGGGCTGTGT
GTGTGTGTGTGTGTGTGTATGTATATGTGTGTGGGTGCACACATCTGTCCCATGTATGCA
GTGAGACCTGTCTACCTCCACAAGGAGCAAGGGCTCTGCCCGCCCTCTGCTCATTCCCTACC
CAGGTAGTGGGACCCCGGGCCCCCTTCTGCCTGGCTTGCCTGCTTCTGCCCTTTCCAGAGGG
GTCTCACTGACAGCCAGAGACAGCAGGAGAAGGGTTGGCTGTGGATCAAGGAAGGCTGCCCC
TGTACCCTGTGGGGAAATGGTGGGTGCATGGCTGGATGCAGAGGTGGAAGGCCCTGGGCCAC
AGGCGAGAGTGGGCGTGTACCTGTCCCAGGTTCCAGCAAGTCTGCAGCTGTGCAGTCCTG
GGGTCCCTGACCCTGTGCGCCAGGGGGCGTGTGTCCAGCAGGGGCCCTGCCTTGCAAGGAA
CGTCTCTCCGGCGGCTGGGCGCTCCTGCCTGGTCTGGGCTGTGTGTGGCGCCCTTTCTCC
TTGTTTGTTCCTCTGTGTCTGTGTGCGTCTAAGCAATAAAGCGTGGCCGTGGGAAAAAA
AA

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FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119516
><subunit 1 of 1, 172 aa, 1 stop
><MW: 18470, pI: 5.45, NX(S/T): 0
MSSSGGAPGASASSAPPAQEEGMTWWYRWLCRLSGVLGAVSCAISGLFNCITIHPLNIAA
GVWMIMNAFILLCEAPFCCQFIEFANTVAEKVDRLRSWQKAVFYCGMAVVPVISLTLT
TLLGNAIAFATGVLYGLSALGKKGDAISYARIQQRQQADEEKLAETLEGEL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

Transmembrane domains:

Amino acids 64-77;109-128

Tyrosine kinase phosphorylation site:

Amino acids 142-150

N-myristoylation sites:

Amino acids 5-11;6-12;9-15;35-41;38-44;46-52;124-130;132-138

Amidation site:

Amino acids 140-144

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FIGURE 23

GTGAAACACCC**ATG**GTTTTATGCTCTATTTCTCTTTTCCCTCATCTTCTTCCACATCCTCTTT
CTGAATGTATCAAACACTTTCCTTGAAGTGGGGCACCAGGAGGGCCACTCCAGTCTCCAATG
CAGGGACTCAGGGGCAGGGATCTCTGAGAAAGTGGCCATCTCGTTATTAAAGCTCTGTCCCTC
TGCTTCCCTCTCACCTCAGAAGCAGCCCGTTTATTCAACAGAGCTCCAGGTTGCCAGCTAGG
GGTTTTCGGGACCATAGACCAAGCAACCCCGAGAGACTGAGTACTGACCTGCAGTTGTTCCAG
AAACTCTGCTGGGAATTAGGTTGTGACCTAGAAGTGAAC**TGA**ACTAACAGTGAGAAGGCAG
GGTAAGAATGCAGTCTAGAGCGCAACCTTTCTCCACTAGACTTGTAAGTAATTTAAGTGAAT
CCTGTCCCCCTGGGGTTCTATCCTGGCTGGCTCTGCTGGTGAAGTTGACTGGCCAGCATAGG
GCACTTGATGAGACCCTGGAATGCTGAGGCCAGTTGGGCAGCAAGCTTTCACCTCATCCTTC
TGCCCATCTATCCAGCCATTCAAACATTCATTTCGCCTGAAGACATTTATCAAGCTCCTGCAA
TGGGTCAGGCATCTGCTAGGCACTGGGGACACAGAGCTCACAGTCTCCTGGAGGGGGTGAGA
GATGACTGACAGGTGGTCTGTGGTGCAGTGTGACCTGGGAATGCACACAGTACTGTGGAAAC
ACGGGAGAGGCATCTAGCACAACTGAGAGGGCCAGGGGAGGCTTCCTGGCAGGTTTCCCTT
TAACCATCTTAAGGGAAAGAGGCCTAGGTAGGAAAATAAAGGCACAGTGGTGTCCCAGACA
GAGGGCACTCTACATGGAA

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FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119530
><subunit 1 of 1, 113 aa, 1 stop
><MW: 12799, pI: 7.53, NX(S/T): 1
MVLCSISLFLIFFHILFLNVSNYFLEVGHQEGHSSLQCRDSGAGISEKVAISLLKLCPLL
PSHLRSSPFIQQSSRLPARGFRDHRPSNPERLSTDQLFQKLCWELGCDLEVN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 19-23

Glycosaminoglycan attachment site:

Amino acids 41-45

N-myristoylation site:

Amino acids 42-48

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FIGURE 25

CGGGCTCCGCGCGGTCCCACTTCCCGGCTCCCTTCGCCTCCAGGATGCGCTGAGCCCTACAA
CACCCCCAGCGGCCCGGGCTCCCCACGAGGTGTGAATGACAGAGGTGGTGCCATCCAGCG
CGCTCAGCGAGGTGAGCCTGCGCCTCCTCTGCCACGATGACATAGACACTGTGAAGCACCTG
TGTGGCGACTGGTTCCCCATCGAGTACCCAGACTCATGGTATCGTGATATCACATCCAACAA
GAAGTTCTTTTCCCTTGCTGCAACCTACAGAGGTGCCATTGTGGGAATGATAGTAGCTGAAA
TTAAGAACAGGACCAAAATACATAAAGAGGATGGAGATATTCTAGCAACCAACTTCTCTGTT
GACACACAAGTCGCGTACATCCTAAGTCTGGGCGTCGTGAAAGAGTTCAGGAAGCACGGCAT
AGGTTCCCTCTTACTTGAAAGTTTAAAGGATCACATATCAACCACCGCCCAGGACCACTGCA
AAGCCATTTACCTGCATGTCTCACCACCAACAACACAGCAATAAACTTCTATGAAAACAGA
GACTTCAAGCAGCACCCTATCTCCCTATTACTACTCCATTTCGAGGGGTCTCAAAGATGG
CTTCACCTATGTCTCTACATCAACGGCGGGCACCCTCCCTGGACGATTTTGGACTACATCC
AGCACCTGGGCTCTGCACTAGCCAGCCTGAGCCCCCTGCTCCATTCCGCACAGAGTCTACCGC
CAGGCCCCACAGCCTGCTCTGCAGCTTCCCTGCCATGGTCGGGCATCTCTTCCAAGAGTGGCAT
CGAGTACAGCCGGACCATGTGATGTCTGGCTGGGCAGCCGCCACCAGGCCCCACCCTTCAGCC
GCCCCGAGAGCCCCGCTTCCCTGTCCATCTGACCCCTTCTGTTTTCTGCAAGGAGCTGCCAGC
CATCTAAGTGGCTCGTGGCCTGCGCAGAGCATGCCCATCCGTGGCAGGCTCTTCAGCTCCCCTCCCT
GCTTCTGGAAACCTCTGCCTGCTGCCCTGGCCCTGCCCCCTGCGCATGCACCATCCCCAGG
GCTGACCCAGTGTGGCTGCATTCACTGGGAGGGGCTGCCCTCACTGGGCCTCTCCCACTCCG
CTGCCCTGTTCTTGCAGCTCCTTCCCTGGAAAGCTGGAGGGGACTTTCTCCTGCAAGGGAGGAA
CGCAAGTATTATGGACACACTTGACCGTAAAGGCACAGGAGCCTCGGAACAAGGGGGCGCAA
TAAAGGGAATGGCCCGTCCCTTCCAGAACCAGCCCAAAGAAGCCTGGGGGGTGAGGAGTGG
CCCCCACTCCTCCATGAGGGGCTGATGAGGGGTGGGCAGCCTGGGGGAGGCTTTCTCGCAA
GCACAGAGCTCTGAGGCTCAGCCCCCTGGCACAGGCGGTACGCATCAGGACGGTTCCTACT
CCTCAGCACCTTCCGTGCAGTTACCAGTGCCCTGGGAGGTCACTGCCCCGTGGACCTTGG
CATGCTCCATTGAGCTGACCTGCTGAGGACAGGCATCGCCGAGACTCCTTGGGTCTCCCCG
CCCTCCCTCATGCTGCCACAAGCTGCTGCTCCAAGGCCTGGCCACATGCAGACAGGAGGAAG
CTGAGCTCGACATTAGGCCTCAAGGCTGCCATCTGTCTTGTAGGGCCTGGCCTTGTGGGCAG
GGGGCAGTCTGTGCCTTGTGGGCCCTCAGCCTCTGAGGGCAGAGATGCTGTGAGTGCCTGCA
GGTGCATCACATACTTCTAGCATCCTCTCCACCTGCATTCCAAATGCTGCTTGCTGCCTGC
CCTGCCCTCCGATGCAGGGGTGGGGTGGGGGGCGGAGTCCCGCCCAGCATAGCTGCAGTGTG
ACAAAGCCATGGCAGAGGGTCTAGCGGCGCCACCCTGCCCCAGCCTGAGGAGGAGGGAGAG
GGAGGAACAACCCTGGGCAGACGGGGTCTCAGGGACCTGTGTCTTCCGCCTCCAGAGCTGC
CCAGCCACGGGCTCTCAGGGTGTGGGGCAGCCCCAGGTCCCCCTTGAACCTCAGCTGGGGC
CAGGGGCCCTCAGAATGAAGGCAGGCACCAGGCAGGAGCAGCATCCCCCTCCTTGACGGTGC
TGGCAGGAGGGCCGCGCCATGCTGACTGCTTGAACCTCTGCTGACCTGACAGTGTGGCGGG
AGGGCCGCACCATGCTGACTGCCTGAATCTCTGCTGAGGCTGCCTGCCTGCCGGGCCAGCT
CAGCGCCCTCTCCACTGCGAATCAGTGGCGATCATGTGATTTCTATTTCTGCCCCACAGGGT
AAGGGACGAGTCTTCTGGAAGGCTCTGCCATGGACATTTGTCTCGGGCTCAGAGGCCCCAC
CCTGCCCCACACCTGCCCCTAATCACTGCAGTGTCCAGCCCAGTGTTGAACAGATTGTAGCG
TTCTGTCTCATTACGAGCAAATAAATAGACTTTCATTGGGAAAAAAAAAAAAA

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FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA121772
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27465, pI: 7.72, NX(S/T): 3
MTEVVPSSALSEVSLRLLCHDDIDTVKHL CGDWFPIEYPDSWYRDITSNKKFFSLAATYR
GAIVGMIVAEIKNRTKIHKEDGDILATNFSVDTQVAYILSLGVVKEFRKHGIGSLLLES
LDHISTTAQDHCKAIYLVLTNTNTAINFYENRDFKQHHYLPYYYSIRGVLKDGFTYVLY
INGGHPPWTILDYIQHLGSALASLSPCSIPHRVYRQAHSLLCSFLPWSGISSKSGIEYSR
TM
```

N-glycosylation sites:

Amino acids 73-77;88-92;143-147

N-myristoylation sites:

Amino acids 61-67;65-71;198-204;235-241

Matrixins cysteine switch motif:

Amino acids 18-31

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FIGURE 27

GTGGGGCAGCAGCCACCCGCTCACCTCCATCCCCAGGACTTAGAGGGACGCAGGGCGTTGGG
AACAGAGGACACTCCAGGCGCTGACCCTGGGAGGCCAGGACCAGGGCCAAAGTCCCGTGGGC
AAGAGGAGTCCTCAGAGGTCTTCATTACGCGGTTCCGGGAGGTCTGGGAAGCCCACGGCCT
GGCTGGGGCAGGGTCAACGCCGCCAGGCCGCCATGGTCTCTGTGCTGGCTGCTGCTTCTGGTG
ATGGCTCTGCCCCCAGGCACGACGGGCGTCAAGGACTGCGTCTTCTGTGAGCTCACCGACTC
CATGCAGTGTCTGGTACCTACATGCACTGTGGCGATGACGAGGACTGCTTCACAGGCCACG
GGGTCGCCCCGGGCACTGGTCCGGTCATCAACAAAGGCTGCCTGCGAGCCACCAGCTGCGGC
CTTGAGGAACCCGTCAGCTACAGGGGCGTCACCTACAGCCTCACCACCAACTGCTGCACCGG
CCGCCTGTGTAAACAGAGCCCCGAGCAGCCAGACAGTGGGGGCCACCACCAGCCTGGCACTGG
GGCTGGGTATGCTGCTTCCTCCACGTTTGCTGTGACCAACAGGGAGGACAGGGCCTGGGACT
GTTCTCCCAGATCCGCCACTCCCCATGTCCCCATGTCTTCCCCACTAAATGGCCAGAGAG
GCCCTGGACAACCTCTTGCGGCCCTGGCTTCATCCCTTCTAAGGCTGTCCACCAGGAGCCCG
GTGCTAGGGGAAGCATCCCCAGGCCTGACTGAGCGGCAGGGGAGCACGGCCCGTGGGTTGA
TTGTATTACTCTGTTCCACTGGTTCTAAGACGCAGAGCTTCTCACATCTCAATCAGGATGCT
TCTCTCCATTGGTAGCACTTTAGAGTCCATGAAATATGGTAAAAAATATATATATATATCATAA
TAAATGACAGCTGATGTTTCATGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125148
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13004, pI: 5.70, NX(S/T): 0
MVLCLLLLLVMALPPGTTGVKDCVFCELTDSMQCPGTYMHCGDDEDCFTGHGVAPGTGPV
INKGCLRATSCGLEEPVSYRGVTYSLTTNCCTGRLCNRAPSSQTVGATTSLALGLGMLLP
PRL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-13

N-myristoylation sites:

Amino acids 19-25;52-58;64-70;81-87;106-112

Ly-6 / u-PAR domain proteins:

Amino acids 84-97

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FIGURE 29

GGCATT TTTGAAAGCCCAGTGT TGCCAGGGGGCATCTCCTTTGTGTTTATGAGAGACCTGCA
TTCTCCCTGGCTCAGTTCTCTCAGGCTCTCCAGAGCTCAGGACCTCTGAGAAGA**ATG**GAGCC
CTCCTGGCTTCAGGAACATCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTCTGCATGTCTC
TGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATCAGAGCCCTGCAC
CTGTTTCCTGCACCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTTTACCCAGTAAAGGA
GTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTTCCCTTGTTGGGTGGAC
CCTTTACGATGTTCTTCAGTGTCATGACCCAGACTATGCCAAGATTCTCCTGAAAAGACAA
GATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGGGTGGTTCGAGGACTTGTGAC
CCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTGAAACCTGGCTTCAACATCAGCA
TTCTGAAAATATTATCACCATGATGTCTGAGAGTGTTTCGGATGATGCTGAACAAATGGGAG
GAACACATTGCCCAAACTCACGTCTGGAGCTCTTTCAACATGTCTCCCTGATGACCCTGGA
CAGCATCATGAAGTGTGCCTTCAGCCACCAGGGCAGCATCCAGTTGGACAGTACCCTGGACT
CATACCTGAAGCAGTGTTCAACCTTAGCAAAATCTCCAACCAGCGCATGAACAATTTTCTA
CATACACAAGCCTGGTTTTTCAAATTCAGTCTCAAGGCCAAATCTTTTCTAAATTTAACCA
AGAACTTCATCAGTTCACAGAGAAAGTAATCCAGGACCGGAAGGAGTCTCTTAAGAGTACGC
TAAAACAAGATACTACTCAGAAAAGGCGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAA
AGCGAAAACACCAAAGATTTCTCTGAAGCAGATCTCCAGGCTGAAGTGAAAACGTTTCATGTT
TGCAGGACATGACACCACATCCAGTGCTATCTCCTGGATCCTTTACTGCTTGGCAAAGTACC
CTGAGCATCAGCAGAGATGCCGAGATGAAATCAGGGAACTCCTAGGGGATGGGTCTTCTATT
ACCTGGGAACACCTGAGCCAGATGCCTTACACCAGATGTGCATCAAGGAATGCCTCCGCCT
CTACGCACCGGTAGTAAACATATCCCGGTTACTCGACAAACCCATCACCTTTCCAGATGGAC
GCTCCTTACCTGCAGGAATAACTGTGTTTATCAATATTTGGGCTCTTCACCACAACCCCTAT
TTCTGGGAAGACCCTCAGGTCTTTAACCCCTTGAGATTCTCCAGGGAAAATCTGAAAAAAT
ACATCCCTATGCCTTCATACCATTCTCAGCTGGATTAAGGAACTGCATTGGGCAGCATTTTG
CCATAATTGAGTGTAAGTGGCAGTGGCATTAACTCTGCTCCGCTTCAAGCTGGCTCCAGAC
CACTCAAGGCCTCCCCAGCCTGTTTCGTCAAGTTGTCCTCAAGTCCAAGAATGGAATCCATGT
GTTTGCAAAAAAAGTTTGCT**TAA**TTTTTAAGTCCTTTTCGTATAAGAATTAATGAGACAATTTTCCT
ACCAAAGGAAGAACAAAAGGATAAATATAATAACAAATATATGTATATGGTTGTTTGACAAA
TTATATAACTTAGGATACTTCTGACTGGTTTTGACATCCATTAACAGTAATTTTAATTTCTT
TGCTGTATCTGGTGAAACCCACAAAAACACCTGAAAAAATCAAGCTGACTTCCACTGCGAA
GGGAAATTATTGGTTTGTGTAAGTAGTGGTAGAGTGGCTTTCAAGCATAGTTTGATCAAAAC
TCCACTCAGTATCTGCATTACTTTTATCTCTGCAAATATCTGCATGATAGCTTTATTCTCAG
TTATCTTTCCCATTAATAAAAAATATCTGCCAAA

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FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125150
><subunit 1 of 1, 505 aa, 1 stop
><MW: 59086, pI: 9.50, NX(S/T): 3
MEPSWLQELMAHPFLLLLCMSLLLFQVIRLYQRRRWIRALHLFPAPPAHWFYGHKEF
YPVKEFEVYHKLMEKYPICAVPLWVGPFMTFFSVHDPDYAKILLKRQDPKSAVSHKILESW
VGRGLVTLTGSKWKKHRQIVKPGFNISILKIFITMMSESVRMMMLNKWEEHIAQNSRLELF
QHVSLMTLDSIMKCAFESHQGSIQLDSTLDSYLKAVFNLSKISNORMNFLHHNDLVFKFS
SQGQIFSKFNQELHQFTEKVIQDRKESLKDCLKQDTPQRRWDFLDILLSAKSENTKDFS
EADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQQRCDREIRELLGDGSSITWEHLS
QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPYFWED
PQVFNPLRFSRENSEKIHPIYAFIPFSAGLRNCIGQHFAIIECKVAVALTLLRFLAPDHS
RPPQPVVRQVVLKSKNGIHVFAKKVC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 451-470

N-glycosylation sites:

Amino acids 145-149;217-221;381-385

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 264-268

N-myristoylation sites:

Amino acids 243-249;351-357;448-454;454-460

Cytochrome P450 cysteine heme-iron ligand signature:

Amino acids 445-455

Cytochrome P450 cysteine heme-iron ligand proteins:

Amino acids 442-473

FAD-dependent glycerol-3-phosphate dehydrogenase proteins:

Amino acids 124-141

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FIGURE 31

TCCGCTGTCGCCCAGTCCCGGCCGCTGGCGGGAAGTACCTGGAGCAAGCAGGACCTTCCCT
CCCACCTCTCCCGCCTGGCCTCCGCGGGAGTCCCCTACGATCCCGCTCAGCAGTGGGGCACT
CGCTGAGGACAGCGAGTCTTGGGAGTGAGCCCAAGGCCACCCCTGGCCAGCCCAGGAGAGAT
AGCCAGGGCAGGCCCAGCAGCCCAGGCCAGGCTCTGGCCACGGCGGTCTCCGACATGGAGA
GACATTGTCTGCTTTTTATCCTGTAACTGTCTTCGGTGGTTGTGCCACGACATTCCCCAG
GGTTCAGGTGCCCGGTGGCCGAGGGTCAGTCCAGTGGTAGAGCCTTGCTCTCCTAGGCTCAT
CCTGCTGGCGGTCTCTGCTTCTGCTGTGTGGTGTACAGCTGGTTGTGTCCGGTTCTGCT
GCCTCCGGAAGCAGGCACAGGCCAGCCACATCTGCCACCAGCACGGCAGCCCTGCGACGTG
GCAGTCATCCCTATGGACAGTGACAGCCCTGTACACAGCACTGTGACCTCCTACAGCTCCGT
GCAGTACCCACTGGGCATGCGGTTGCCCCCTGCCCTTTGGGGAGCTGGACCTGGACTCCACGG
CTCCTCCTGCCTACAGCCTGTACACCCCGGAGCCTCCACCCTCCTACGATGAAGCTGTCAAG
ATGGCCAAGCCCAGAGAGGAAGGACCAGCACTCTCCAGAAACCCAGCCCTCTCCTTGGGGC
CTCGGGCCTAGAGACCACTCCAGTGCCCCAGGAGTCGGGCCCCAATACTCAACTACCACCTT
GTAGCCCTGGTGCCCCCTTGAAGGAGGTAGGAGAACGGACCAGAGCTTGGAGAACTAATGCTT
GGAGCCAAGGGCCCCAGCCCACCCACCGTCCCACACATTGCTGTGGCCCCAACCTCGGTGC
CATGTTACACCGGCCCTGGCGTCACCCACTAGGCAGGCTGCTGCTTTCAGCCTCAGCCCCCT
GGCCCAGCCCCAGCAGGCCCTCAGCCTGGAAGAGGCCCTTGGGCCTAAGCCTCGGGTGGGA
GCTCAGGGCCACCTGTGACGTCTGCATCTTCTTGGAGAGAGAATAAAGTTTGTATTTAAGTGGT

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FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125151
><subunit 1 of 1, 194 aa, 1 stop
><MW: 20882, pI: 6.44, NX(S/T): 0
MERHCLLFILLTCLRWLCHDIPQGSGARWPRVSPVVEPCSPRLILLAVLLLLLLCGVTAGC
VRFCCLRKQAAQAPHLPPARQPCDVAVIPMDSDSPVHSTVTSYSSVQYPLGMRLPLPFGE
LDLDSTAPPAYSPLYTPEPPPSYDEAVKMAKPREEGPALSQKPSPLL GASGLETPVPQES
GPNTQLPPCSPGAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 39-58

N-myristoylation site:

Amino acids 55-61

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 50-61

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FIGURE 33

CCTTGCTTGGTGCTTGGCACACACAAATCCAGTGGGCTACACAGGTTTTCCAGAAGCCCCAC
GAGGTGGTA**ATGGT**GCTGCTGATTGAGACCCTGGGGGGCCCTCATGCCCTCGCTGCCCTCCTG
CCTCAGCAACGGCGTGGAGAGGGCAGGGCCCGAGCAGGAGCTCACCAGGCTGCTGGAGTTCT
ACGACGCCACCGCCCACTTCGCCAAGGGCTTGGAGATGGCACTGCTCCCCACCTACATGAA
CACAACTCTGGTAAAAGTCACGGAGCTGGTGGATGCTGTGTATGATCCATACAAACCTACCAG
CTGAAGTATGGCGACATGGAAGAGAGCAACCTCCTCATCCAGATGAGTGCTGTGCCTCTGGA
GCATGGGGAAGTGATTGACTGTGTGCAGGAGCTGAGCCACTCCGTGAACAAGCTGTTTGGTC
TGGCGTCTGCAGCCGTTGACAGATGCGTCAGATTCACCAATGGCCTGGGGACCTGCGGCCTG
TTGTGAGCCCTGAAATCCCTCTTTGCCAAGTATGTGTCTGATTCACCAGCACTCTCCAGTC
CATACGAAAGAAGTGCAAACTGGACCACATTCTCCCAACTCCCTCTTCCAGGAAGATTGGA
CGGCTTTTCAGAACTCCATTAGGATAATAGCCACCTGTGGAGAGCTTTTGCGGCATTGTGGG
GACTTCGAGCAGCAGCTAGCCAACAGGATTTTGTCCACAGCTGGGAAGTATCTATCTGATTC
CTGACGCCCCCGGAGCCTGGCTGGTTTTTCAGGAGAGCATCTTGACAGACAAGAAGAACTCTG
CCAAGAACCAATGGCAAGAATATAATTACCTCCAGAAAGATAACCCTGCTGAATATGCCAGT
TTAATGGAAATACTTTATACCCTTAAGGAAAAAGGGTCAAGCAACCACAACCTGCTGGCTGC
ACCTCGAGCAGCGCTGACTCGGCTTAACCAGCAGGCCCCACCAGCTGGCTTTCGATTCCGTGT
TCCTGCGCATCAAACAACAGCTGTTGCTTATTTTCGAAGATGGACAGCTGGAATACGGCTGGC
ATCGGAGAAACCTCACAGATGAACTGCCCCGCTTTAGTCTCACCCCTCTCGAGTACATCAG
CAACATCGGGCAGTACATCATGTCCCTCCCCCTGAATCTTGAGCCATTTGTGACTCAGGAGG
ACTCTGCCTTAGAGTTGGCATTGCACGCTGGAAAGCTGCCATTTCTCCTGAGCAGGGGGAT
GAATTGCCCCGAGCTGGACAACATGGCTGACAACCTGGCTGGGCTCGATCGCCAGAGCCACAAT
GCAGACCTACTGTGATGCGATCCTACAGATCCCTGAGCTGAGCCCACACTCTGCCAAGCAGC
TGGCCACTGACATCGACTATCTGATCAACGTGATGGATGCCCTGGGCCTGCAGCCGTCCCGC
ACCCTCCAGCACATCGTGACGCTACTGAAGACCAGGCCTGAGGACTATAGACAGGTCAGCAA
AGGCCTGCCCCGTCGCTGGCCACCACCGTGGCCACCATGCGGAGTGTGAATTAC**TGACCCC**
ACCACACACCGGACCACCAAGAGAGCCAGGGCTGCTGTTTCGTGACTCACCAGCACAGATTT
GCTCAGAACTCTGCCCAAGATTGGGCAGAAGTTACTTTAAAAAGACTTGGTTTCAGCTGGTC
ACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGCCAGATGGATCATGAGGCC
AGGAGTTCGAGACCAGCCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAAT
TAACAGCAGAGCGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGACTTGGTTTCATTTGTATAA
TCAAAAAGAGTTGTAAATTAAAGATGTATTATTTATCAGAGAAGACTTTTTAGATAATTTTT
TTAAAGGATCAGATCTTGAAAATGGAATAAATAACTACTGTGAAATGCAAAA

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FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125181
><subunit 1 of 1, 491 aa, 1 stop
><MW: 54759, pI: 5.61, NX(S/T): 0
MVLIIQTLGALMPSPCLSNNGVERAGPEQELTRLLEFYDATAHFAKGLEMA LLPHLHEH
NLVKVTELVDVYDPYKPYQLKYGDMEESNLLIQMSAVPLEHGEVIDCVQELSHSVNKL F
GLASAAVDRCVREFTNGLGTCGLLSALKSLFAKYVSDFTSTLQSIKKCKLDHIPNSLFQ
EDWTAFQNSIRIIATCGELLRHCGDFEQQLANRILSTAGKYLSDCSPRSLAGFQESILT
DKKNSAKNPWQEYNYLQKDNPAEYASLMEILYTLKEKGSSNHNLLAAPRAALTRLNQQA H
QLAFDSVFLRIKQQLLLISKMDSWNTAGIGETLTDELPAFSLTPLEYISNIGQYIMSLPL
NLEPFVQTQEDSALELALHAGKLPFPPEQGDELPELDNMADNWLGS IARATMQTYCDAILQ
IPELSPHSAQLATDIDYLINVMDALGLQPSRTLQHI VTLTKTRPEDYRQVSKGLPRRLA
TTVATMRSVNY
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 242-246

N-myristoylation sites:Amino acids 22-28; 48-54; 121-127; 136-142; 141-147; 328-334;
447-453**Leucine zipper pattern:**

Amino acids 295-317

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FIGURE 35

GCAAGTGCCACCATGCTAGTGTGATTTGGACTTCAGTAAAAGTTAGTTTGCTTCCTTCCCGT
TGTCCCATCTCACTCCTGGGCCACCC**ATG**GGGCTGCTGGTAGCTGGTGTGTGGCTGCTGCTG
GACTGTGTGGCAGTCCATCCATCTGTCTCAGCAGCCACTGCGGGCCTACTTGCTGGGTGCCAG
CACCGCACTCACCCTGCAGGCGTGGCCAGGAGCGTGAGATCCCCAGAGCCCATGGCCAGTG
AGAGGCGGCCAGGGATAGGTACCCAGGGAATGCCACAGGAGTTTGCTGGGCTCACGGAGCTC
TTTCACTGGTCAGAGAGGAGTGTGTGTAGGAGAGGACTTCTACTTGGTGTGAAGGACAGAT
GGGGTTTGGCTGGGAGAGAGGAGGAATGTGGGCGGGCCTTATAGGCAGGCGAGAAGGTGAGA
GCCAAGGCCCTCTGTGGGCAGGGCGAGGTGGCGTGTTGAGGAGACTCGTCCAGCTGGGCAGA
GGCTCATGT**TGA**GGGATGAGGCAGAGCTGGGGGAGGAGGGAGCCCAGAAATGGCAGGTCCTT
GAATGCAGGTTTGGGAAGCAGGGACGCCCTGTGAGGGTACAGAGTCTGGGCTGTTACCTTCTG
TGGCTTTTGCTAGAAAGGTGAGATGTCAGGGAGGAAGACAGGACTCCAGGATGTCTCCTGTCTCT
CTCTGGAAAAAGGAGGTGGGCCCTTTCTCAGCAGTCAGCTGCTGTTTTTGAGGTCTTCTCC
ATGGATAATCCACGGTGTGGGAAGTGGTTAAGGTAATGGATCCTCATGGGCTTACCATAAAA
ATATCTGGAGGCTGGACCATTTTCCTTAAAACGTTATAAAAGCTGGAATTGAATGCCATCGG
TGTCACCCCTGGGAAGTGTGCTTTCTCTTGAGCTCTTTTGGCCCCGAGATAGCAGTCACTCC
ATAGTTTCGTGAAGACCAGCCTGGTGTTCCTGGTTTTCTGCCATTAGGGAGCAGCTAGAGG
TCTTCCAGTAGCTCCTGTGTAAAGTGATGAAAGAAAAGGGCTGGGTGCTGACTGCTCCTGGA
GAAAAGCAACACACTCCCAAAGTCTTAATTGCCTGCTTCCAGGGAGCTGTGGTGGTTTCCCT
TGGGCAGGGCACACGCCCCAGTGGTTGACTTAATAAGGATACATTTTAATCAGAGGACAAAA
ATGTGCCCTGACTTGATTTCCGCATGGGCTTCCAGCATGGTCAAAGG

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FIGURE 36

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125192
><subunit 1 of 1, 139 aa, 1 stop
><MW: 14841, pI: 9.20, NX(S/T): 0
MGLLVAGVWLLLDCAVHPSVSSHCGPTCWVPSTALT TAGVARSVRSPEPMASERRPGIG
TQGM PQEFAGL TELFHWSE RSVCR RGLLLGVEGQM GFGW ERGGMWAGLIGRREGESQG PL
WAGRGGVLRRLVQLGRGSC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 2-8;40-46;86-92;102-108;103-109

Amidation site:

Amino acids 109-113

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FIGURE 37

GGCCAGGAATGGGGTCCCCGGGCATGGTGCTGGGCCTCCTGGTGCAGATCTGGGCCCTGCAA
GAAGCCTCAAGCCTGAGCGTGCAGCAGGGGCCCCAAGTTGCTGCAGGTGAGGCAGGGCAGTCA
GGCGACCCTGGTCTGCCAGGTGGACCAGGCCACAGCCTGGGAACGGCTCCGTGTAAAGTGGACA
AAGGATGGGGCCATCCTGTGTCAACCGTACATCACCAACGGCAGCCTCAGCCTGGGGGTCTG
CGGGCCCCAGGGACGGCTCTCCTGGCAGGCACCCAGCCATCTCACCCCTGCAGCTGGACCCTG
TGAGCCTCAACCACAGCGGGGCGTACGTGTGCTGGGCGGCCGTAGAGATTCTGAGTTGGAG
GAGGCTGAGGGCAACATAACAAGGCTCTTTGTGGACCCAGATGACCCACACAGAACAGAAA
CCGGATCGCAAGCTTCCCAGGATTCCTCTTCGTGCTGCTGGGGGTGGGAAGCATGGGTGTGG
CTGCGATCGTGTGGGGTGCCTGGTTCTGGGGCCGCCGAGCTGCCAGCAAAGGGACTCAGGA
AATGCATTCTACAGCAACGTCCTATACCGGCCCCGGGGGGCCCCAAGAAGAGTGAGGACTG
CTCTGGAGAGGGGAAGGACCAGAGGGGCCAGAGCATTATTCAACCTCCTTCCCGCAACCGG
CCCCCGCCAGCCGCACCTGGCGTCAAGACCCTGCCCCAGCCCGAGACCCTGCCCCAGCCCC
AGGCCCCGGCCACCCCGTCTCTATGGTCAGGGTCTCTCCTAGACCAAGCCCCACCCAGCAGCC
GAGGCCAAAAGGGTTCCCCAAAGTGGGAGAGGAGTGAAGAGATCCCAGGAGACCTCAACAGGA
CCCCACCCATAGGTACACACAAAAAAGGGGGGATCGAGGCCAGACACGGTGGCTCACGCCTG
TAATCCCAGCAGTTTGGGAAGCCGAGGCGGGTGAACACTTGAGGTGAGGGGTTTGAGACCA
GCCTGGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAG
CCTGGGCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAACAAAAAGCAGGAGGATTGGGAGCC
TGTCAGCCCCATCCTGAGACCCCGTCCTCATTTCTGTAATGATGGATCTCGCTCCCACTTTC
CCCCAAGAACCTAATAAAGGCTTGTGAAGAAAAAAAAAAAAAAAAA

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FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125196
><subunit 1 of 1, 278 aa, 1 stop
><MW: 30319, pI: 9.21, NX(S/T): 3
MGSPGMVLGLLVQI WALQEASSLSVQQGPNLLQVRQGSQATLVCQVDQATAWERLRVKWT
KDGAILCQPYITNGSLSLGVCGPQGRLSWQAPSHLTQLDPVSLNHSGAYVCWAAVEIPE
LEEAEGNITRLFVDPDDPTQNRNRIASFPGFLFVLLGVGSMGVAAIVWGAWFWGRRSCQQ
RDSGNAFYSNVLYRPRGAPKKSEDCSGEGKDQRGQSIYSTSFPPQAPRQPHLASRPCPSP
RPCPSRPGHPVSMVRVSPRPSPTQQPRPKGF PKVGEE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

Transmembrane domain:

Amino acids 149-166

N-glycosylation sites:

Amino acids 73-77;105-109;127-131

Glycosaminoglycan attachment site:

Amino acids 206-210

N-myristoylation sites:

Amino acids 5-11;37-43;63-69;108-114

Amidation site:

Amino acids 173-179

FIGURE 39

[illegible]

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FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125200
><subunit 1 of 1, 290 aa, 1 stop
><MW: 32335, pI: 5.82, NX(S/T): 1
MPLLTLYLLLEFWLSGYSIATQITGPTTVNGLERGS�TVQCVYRSGWETYLKWWCRGAIWR
DCKILVKTSQSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT
VQVTIDPAPVTQEETSSSPILTGHHLDNRHKLLKLSVLLPLIFTILLLLLVAASLLAWRM
MKYQQKAAGMSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA
SLPKEDISYASLTGAEQDEPTYCNMGHLSSHLPGRGPPEEPTYSTISRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domain:

Amino acids 155-174

N-glycosylation site:

Amino acids 88-92

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 218-222

Tyrosine kinase phosphorylation site:

Amino acids 276-285

N-myristoylation sites:

Amino acids 30-36;109-115;114-120

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FIGURE 41

AAGAACACTGTTGCTCTTGGTGGACGGGCCCAGAGGAATTCAGAGTTAAACCTTGAGTGCCT
GCGTCCGTGAGAATTCAGCATGGAATGTCTCTACTATTTCTGGGATTTCTGCTCCTGGCTG
CAAGATTGCCACTTGATGCCGCCAAACGATTTTCATGATGTGCTGGGCAATGAAAGACCTTCT
GCTTACATGAGGGAGCACAATCAATTAAATGGCTGGTCTTCTGATGAAAATGACTGGAATGA
AAAACCTCTACCCAGTGTGGAAGCGGGGAGACATGAGGTGGAAAACTCCTGGAAGGGAGGCC
GTGTGCAGGCGGTCTTGACCAGTGACTCACCAGCCCTCGTGGGCTCAAATATAACATTTGCG
GTGAACCTGATATTCCTTAGATGCCAAAAGGAAGATGCCAATGGCAACATAGTCTATGAGAA
GAACTGCAGAAATGAGGCTGGTTTATCTGCTGATCCGTATGTTTACAACCTGGACAGCATGGT
CAGAGGACAGTGACGGGGAAAATGGCACC GGCCAAAGCCATCATAACGTCTTCCCTGATGGG
AAACCTTTTTCTCACCACCCCGGATGGAGAAGATGGAATTTTCATCTACGTCTTCCACACACTT
GGTCAGTATTTCCAGAAATGGGACGATGTTTCAGTGAGAGTTTCTGTGAACACAGCCCAATGT
GACACTTGGGCCTCAACTCATGGGAAGTGACTGTCTACAGAAGACATGGACGGGCATATGTTT
CCATCGCACAAAGTGAAGATGTGTACGTGGTAACAGATCAGATTCCCTGTGTTTGTGACTATG
TTCCAGAAGAACGATCGAAATTCATCCGACGAAACCTTCCTCAAAGATCTCCCCATTATGTT
TGATGTCTGATTCATGATCCTAGCCACTTCCTCAATTATTCTACCATTAACTACAAGTGGA
GCTTCGGGGATAATACTGGCCTGTTTGTTCACCAATCATACTGTGAATCACACGTATGTG
CTCAATGGAACCTTCAGCCTTAACCTCACTGTGAAAGCTGCAGCACCAGGACCTTGTCCGCC
ACCGCCACCACCACCCAGACCTTCAAAAACCCACCCCTTCTTTAGCAACTACTCTAAAATCTT
ATGATTCAAACACCCACAGGACCTACTGGTGACAACCCCTGGAGCTGAGTAGGATTCCTGAT
GAAACTGCCAGATTAACAGATATGGCCACTTTCAGCCACCATCACAATTGTAGAGGGAAT
CTTAGAGGTTAACATCATCCAGATGACAGACGTCTGATGCCGGTGCCATGGCCTGAAAGCT
CCCTAATAGACTTTGTGCTGACCTGCCAAGGGAGCATTCCACGGAGGTCTGTACCATCATT
TCTGACCCACCTGCGAGATCACCCAGAACACAGTCTGCAGCCCTGTGGATGTGGATGAGAT
GTGTCTGCTGACTGTGAGACGAACCTTCAATGGGTCTGGGACGTACTGTGTGAACCTCACCC
TGGGGGATGACACAAGCCTGGCTCTCACGAGCACCCCTGATTTCTGTTCTGACAGAGACCCA
GCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGATCTCCGTTGGCTGCTTGGCCATATTTGT
CACTGTGATCTCCCTCTTGGTGTACAAAAACACAAGGAATACAACCCAATAGAAAATAGTC
CTGGGAATGTGGTCAGAAGCAAAGGCCTGAGTGTCTTTCTCAACCGTGCAAAGCCGTGTTT
TTCCCGGAAACCAGGAAAAGGATCCGCTACTCAAAAACCAAGAATTTAAAGGAGTTTCTTA
AATTTTCGACCTTGTTTCTGAAGCTCACTTTTCAGTGCCATTGATGTGAGATGTGCTGGAGTG
GCTATTAACCTTTTTTTTCTAAAGATTATTGTTAAATAGATATTGTGGTTTGGGGAAGTTGA
ATTTTTTATAGGTTAAATGTCATTTTAGAGATGGGGAGAGGGATTATACTGCAGGCAGCTTC
AGCCATGTTGTGAAACTGATAAAAGCAACTTAGCAAGGCTTCTTTTTCATTATTTTTTATGTT
TCACTTATAAAGTCTTAGGTAAGTAGTAGGATAGAAACACTGTGTCCCGAGAGTAAGGAGAG
AAGCTACTATTGATTAGAGCCTAACCCAGGTTAACTGCAAGAAGAGGCGGGATACTTTTCAGC
TTTCCATGTAACCTGATGCATAAAGCCAATGTAGTCCAGTTTCTAAGATCATGTTCCAAGCTA
ACTGAATCCCACCTTCAATACACACTCATGAACCTCTGATGGAACAATAACAGGCCCAAGCCT
GTGGTATGATGTGCACACTTGCTAGACTCAGAAAAATACTACTCTCATAAATGGGTGGGAG
TATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATATATTCATTTA
TTCCATGGACATTTAGTTAGTGCTTTTTATATACCAGGCATGATGCTGAGTGACACTCTTGT
GTATATTTCAAATTTTGTACAGTCGCTGCACATATTTGAAATCATATATTAAGACTTTCC
AAAGATGAGGTCCTGGTTTTTCATGGCAACTTGATCAGTAAGGATTTACCTCTGTTTGTA
ACTAAAACCATCTACTATATGTTAGACATGACATTCTTTTTCTCTCCTTCCTGAAAAATAAA
GTGTGGGAAGAGACA

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FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125214
><subunit 1 of 1, 572 aa, 1 stop
><MW: 63953, pI: 6.55, NX(S/T): 12
MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMREHNQLNGWSSDENDWNEKLYP
VWKRGRDMRWKNSWKGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIVYEKNC
RNEAGLSADPYVYNWTAWSESDSGENGTGQSHHNVFPDGKPFPHHPGWRRWNFIYVFHTL
GQYFQKLGRCSVRVSVNTANVTLGPQLMEVTVYRRHGRAYVPIAQVKDVYVVTDQIPVFV
TMFQKNDRNSSDETFLKDLPIMFVDLIHDPESHFLNYSTINYKWSFGDNTGLFVSTNHTVN
HTYVLNGTFSLNLTVKAAAPGPCPPPPPPRPSKPTPSLATTLKSYDSNTPGPTGDNPLE
LSRIPDENCQINRYGHFQATITIVEGILEVNI IQMTDVLMPVPWPPESSLIDFVVTCQGS
PTEVCTIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTS
TLISVPDRDPASPLRMANSALISVGCLAIFFTVISLLVYKKHKEYNPIENSPGNVVRSG
LSVFLNRAKAVFFPGNOEKDPLLKNOEFFKGV
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 496-516

N-glycosylation sites:

Amino acids 93-97;134-138;146-150;200-204;249-253;275-279;
296-300;300-304;306-310;312-316;459-463;467-471

N-myristoylation sites:

Amino acids 91-97;147-153;290-296;418-424

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 496-507

Cell attachment sequence:

Amino acids 64-67

FIGURE 43

[illegible]

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FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125219
><subunit 1 of 1, 283 aa, 1 stop
><MW: 31175, pI: 7.51, NX(S/T): 0
MADPHQLFDDTSSAQSRGYGAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSSLAAQ
GKELVDKNIDRFIPITKLKYYFAVDTRYVGRKLGLLFFPYLHQDWEVQYQQDTPVAPRFD
VNAPDLYIPAMAFITYVLVAGLALGTQDRFSPDLLGLQASSALAWLTLEVLAILLSLYLV
TVNTDLTTIDLVAFLGYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLKI
LADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFFHLVR
```

Important features of the protein:**Transmembrane domain:**

Amino acids 126-142;164-179;215-233

N-myristoylation sites:

Amino acids 54-60;141-147;156-162;201-207;205-211;209-215

Amidation site:

Amino acids 89-93

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FIGURE 45

GCTGAGCACCAACAGGAACTATTCCAGTGAAGAGCAAGTGCTGCCCGACCCAGGACCCTGTG
CCAGGCTGGCAGCCCTCCAGCTCCCTCCAGAGAGGAAACCTCTGTCTGGCTGAGGGTGGGAC
TAGCTGGG**ATG**TCTCACTCCAGTTGCTCAGGTTACCCAGGAAGCTCCTCCGTGGAGTGGCC
AGCCTGATTCTAGCCCTGTCTCTCTGGCAGCACATGCCACACCTGCCTGGGCCTTCTGCTC
CCTGATGCTTGATGAGCCCTGCCTCCTCAATGTTTCTCAAAGACAGACCCCCCTGAGGCCAGC
TTGAATGTGAAGACTGCTGAAGTCAGCTGGCTTCACTTGAGCTGCAGAAAAGGTGGCTGGGA
TGGCCCAGGTGCACCCAGAGGCCCCAGCCCTTTGGCTGCCTTTGGGT**TGA**CTTGGGTGT
CTCTGAGGCCCTGCCAGAGCTGGGCCTGCGGGTGGTGGGCGGTCCGACCTCGGGCAGTCAGT
GCTCCGCAGCCTCAGCACTGCATCCCAGACCCAGTGTCCTCAGAGGGAAGAGCCAGCCTCCC
TGCCTCATGGAACCAGGAGTCCCAAAAAGTCAGGAGCCTGGAGGCTCTGAAAGGAGCAGGGA
TTCCATAGTGC GTGAAGCTGAAATAGGCGCCCTCCTGGGGAGCCCCAGCAAACTGTTTTT
CATACCCACTCCCAGAACTGCCCCGCTCCAGCTCCAGCGCCAGCGCCAGCTGGTTGCCAGGC
GTCATTGGAGAGGCCTGGCTGCCCCAGGGGCAGCAGGGAGTGGTGGACCTGTATGGGCTGGC
AGGAGGCCATTGGCCATGCTGACAAGTGTACCTGCCTTCCTAGCCTGGAGCCACCCCTCAG
GTGGCCTGCTTGACCTCCTATCCGGAGGTAGCCTGCCCCACCTGTAGGCAGAGGGGGCTCT
TGCTTGAGGCCTGCACAGGAAGCAAGTATAGCCCCGGTGCCCCAGAGTGGGTCCACTTAGC
CCTGGCGAGATGGCCTGTCCTGAGATCTCTGCTCCAGACCCACCATCTGGGGAGCACAGT
CCTTAGGCTGCCTGGTCCAGGAAGGGGTGCGGCTCTGTGTCAGGAAACCTGGACTCTCAAGGC
CCACCAGCCTCTCCGTGAGTGTTAGAAATCACAGATACAGTATATACTTAATTACACTACTC
ACTACTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 46

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA128309
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10112, pI: 8.64, NX(S/T): 0
MSHSSCSGSPRKLLRGVASLILALSSLAHATPAWAFCSLMLDEPLPPQCFSKTDPPPEAS
LNVKTAEVSWLHLSCRKGGWDGPGAPRGPSPLAAFG
```

Important features of the protein:

Signal peptide:

Amino acids 1-31

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FIGURE 47

TTCCGGGGCCCTGGCGTCTCGTCTCCTTACCCTGGGGCTACCCTTGCCCCGGTCCTACTGCCCG
CGGTAAACCCGCCGCGAGCCGCCTCTCCCCTCCCCGCCGACTCAACCCTGCCCTCCCCCGT
GCTTTGCAGACGCCGCCCGGGGGCCCAGGCGGCTGATGCGTGTGGGCCTCGCGCTGATCTTG
GTGGGCCACGTGAACCTGCTGCTGGGGGCCGTGCTGCATGGCACCGTCCTGCGGCACGTGGC
CAATCCCCGCGGCGCTGTCACGCCGGAGTACACCGTAGCCAATGTCATCTCTGTFCGGCTCGG
GGCTGCTGAGCGTTTCCGTGGGACTTGTGGCCCTCCTGGCGTCCAGGAACCTTCTTCGCCCT
CCACTGCACTGGGTCCTGCTGGCACTAGCTCTGGTGAACCTGCTCTTGTCCGTTGCCTGCTC
CCTGGGCCTCCTTCTTGCTGTGTCACTCACTGTGGCCAACGGTGGCCGCCGCCCTTATTGCTG
ACTGCCACCCAGGACTGCTGGATCCTCTGGTACCACTGGATGAGGGGCCGGGACATACTGAC
TGCCCCCTTTGACCCCAACAAGAATCTATGATACAGCCTTGGCTCTCTGGATCCCTTCTTTGCT
CATGTCTGCAGGGGAGGCTGCTCTATCTGGTTACTGCTGTGTGGCTGCACTCACTCTACGTG
GAGTTGGGCCCTGCAGGAAGGACGGACTTCAGGGGCAGCTAGAGGAAATGACAGAGCTTGAA
TCTCCTAAATGTAAAAGGCAGGAAAATGAGCAGCTACTGGATCAAAATCAAGAAATCCGGGC
ATCACAGAGAAGTTGGGTTTAGGACAGGTGCTGTTCCGAGACTCAGTCCTAAAGGGTTTTTT
TTCCCACTAAGCAAGGGGCCCTGACCTCGGGATGAGATAACAAATTGTAATAAAGTAACTTC
TCTTTTCTTCTAAA

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FIGURE 48

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129535
><subunit 1 of 1, 222 aa, 1 stop
><MW: 23566, pI: 6.70, NX(S/T): 0
MRVGLALILVGHVNLLLGAVLHGTVLRHVANPRGAVTPEYTVANVISVGSGLLSVSVGLV
ALLASRNLLRPPLHWVLLALALVNLLLSVACSLGLLLAVSLTVANGRRRIADCHPGLLD
PLVPLDEGPGHDTDCFPDPTRIDYDTALALWIPSLMSAGEAALSGYCCVAALTLRGVGPCR
KDGLOQGLEEMTELESPKCKRQENEQLLDQONQEIRASQRSWV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 44-60;76-96

N-myristoylation sites:

Amino acids 94-100;175-181

Amidation site:

Amino acids 106-110

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 81-92

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FIGURE 49

CGTCAGTCTAGAAGGATAAGAGAAAGAAAGTTAAGCAACTACAGGAAATGGCTTTGGGAG
TTCCAATATCAGTCTATCTTTTATTCAACGCAATGACAGCACTGACCGAAGAGGCAGCCG
TGAAGTTCTCACACCTTTCCTGGAAGATCATAACAGTTACTGCATCAACGGTGCTTGTG
CATTCCACCATGAGCTAGAGAAAGCCATCTGCAGGTGTTTTACTGGTTATACTGGAGAAA
GGTGTGAGCACTTGACTTTAACTTCATATGCTGTGGATTCTTATGAAAAATACATTGCAA
TTGGGATTGGTGTGGATTACTATTAAGTGGTTTTCTTGTTATTTTTTACTGCTATATAA
GAAAGAGGTATGAAAAAGACAAAATATGAAGTCACTTCATATGCAATCGTTTGACAAATA
GTTATTCAGGCCCTATAATGTGTCAGGCACTGACATGTAAAATTTTTTAAATTAATAAAG
AGCTGTAATCTGGCAAAAAGTTTCTATGTAATATTTTTCATGCCTTTTCTCATAAACCCA
GACGAGTGGTAAAAATTTGCCTTCAGTTGTAATAGGAGAGTTCAAACGTACAGTCTCCCT
TCAACCTATCTCTGTCTGCCCATATCAAAATTATAAATGAGGAGGACAGCAGGCCCAAG
AAAGTAGGGACTAAGTATGTCTTGTTCAAATTGTATATTCAGTGACTTACACTATGCCT
AGCACACAACACACACTGAGTAAATATTTGTTGAGTGAAATAAAATCAAGAAACAAGTAA
AAACTGA

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FIGURE 50

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129549
><subunit 1 of 1, 133 aa, 1 stop
><MW: 14792, pI: 5.97, NX(S/T): 0
MALGVPISVYLLFNAMTALTEEA AVTVTPPITAQQADNIEGP IALKFSHLCLEDHNSYCI
NGACAFHHELEKAICRCFTGYTGERCEHLTLTSYAVDSYEKYIAIGIGVGLLLSGFLVIF
YCYIRKRYEKDKI
```

Important features of the protein:**Signal peptide:**

1-20 (weak)

Transmembrane domain:

103-117

N-myristoylation site.

4-10;106-112;110-116

EGF-like domain cysteine pattern signature.

75-87

Integrins beta chain cysteine-rich domain proteins

66-88

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FIGURE 52

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129580
><subunit 1 of 1, 114 aa, 1 stop
><MW: 12886, pI: 7.04, NX(S/T): 0
MQIQNNLFCCYTVMSAIFKWLLLYSLPALCFLLGTOESESFHSKAEILVTLNQVIISPA
GPHALTWTTHFSPSVIIILVPCWWHAVIVTQHPVANCYVTNHLNIQWLELKAGS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-33

Transmembrane domain:

Amino acids 71-86

N-myristoylation site:

Amino acids 35-41

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FIGURE 53

TTTTGAAATGGTTT**ATG**ACCTCTTCCCCACTTCCCCGCTTGCTTTGCTCATTAGTGTTCCCTA
GGTGGCTGCTGGGTGACGGGCTTTTCATCATCTCTGATGTGGGCCAGTGCGAAAGAGCAGCT
GCAACATCTGTTTCTAATTGGGTCGTGCCTTTATAAATACTTCTTGCCATTTTGTCACATTG
CTTCCCTCCCACCTGTCTTCCTTGGAGTACTGCAGAATCTGTAAGCGTCCCTGGAATGCAC
ACGTGGACCTTGTCATTCCCAAACAGACTTTCTGCTGGTCAGCACTTTGTAATGTTCCGGCTG
TTACAGGCAT**TAG**TCACCTTGCTCAGAGAGAGACTGTGGTCTTTGGAAACTGAAGAAAATGTC
TTTTTTGTTGTTGTTAATTCTTGGCATCCAGTTAGATTTAACTTCTCAAGAGTTTACACAGA
CTTTTAGAAAAACATTCTGTCTCTAAGAAAAAAGTGCTCTAGCTTTGTACAGTTTTTGGATT
TTCACACTTGGTGGTTGTTTGCTGAAATGCTGTTTTGCTAGTGATCCCCCTCCTCCCCCTAT
CTGGGGTTGTAAGCAGCTCTGGGGCTCTGTTCACTTCGGATACCTGTTTCTGGGGACTGCTT
TTCAACAGCGTTTTTCCTAAGGGCATATGAGAAATTTAATTTCTGATGGAATGAAGGTGAAA
CTCTAGTCCCAGGTAAACCTGGGTAGGCTGTAGAGACAGAAAGGGGGCTGCAGGTCTAGGTG
GAAGAACGAGAACGAATGCAGCATGGTATTTCCAGGCCTTTTAGATTCGGCTTCATCCACAA
CCAATGTGAGTTCTTATCTGCAAAGCGGGCCTAAGTGTAATGGAGGGAAGGTGGGCCAGGCA
CCAGGGTCCTGGGTTCTCCCGCGCCTCACTCTGTCTCCACCTGGCCCATGCATAAAGAACAC
TAGTCAAGTAGCCATTGTACCTGTTTCCTTATCTGAAAATGAGAAGGTTGGAGAGTATGACT
TCTGTTGAAACAACAAGGCGCTTACAAATTTTGGTGAAGTCGAATGAGGGCAGCGTTAAGAG
AAATATCAAAGTTAGTCATTGGATTTTCAGGGCTTAGGGATGGAACCAGCTGGTAGTAGACT
GGTTGTAGTTATGTCCAAGGGCAGAGTGGGAAAAATTTGGCCGAAAAGAGTGTGGTGGGTG
ACCAGCAAATGTTAGAGGTATACATCAGGGCACAGAGGAGAAAAGCTAACATGATACTGATG
ACTTCAAGTCTTCACTGTCCAATTCAGAGGATAGGGGAGGGTTTAAGCTGATTAAACAGTGG
GCTTTTTTTCTCCTGCAAGAGGGTGGAGGTCTATAACTGTGCAGATTTTATCAGATGCATGC
TAATACATGTTATTCTGGGGGACTCTCTTATACCTTGAAGTAGACATTGCTGCTATTTGCGT
GAAAAAATAGGAGGACTTATTTGAATTGAGAATGGGGATAGGCTGAGTTCACCCGAGATGT
TGGCTTAGAGATGCCTGGGCCATGCTGTACAGTAGGAAGCCCAGCAGAGGAGATTGGGCTGT
GTGGGTCATGACAAAGGGAGTTGTTAGCTTATGGTTGGCTATTAAAGTCATGGGCAAGGATG
GGCAAGAAAAGTGTGTAAAATGAGCTGACAAAAGATAAATATGTTAATTA

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FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129794
><subunit 1 of 1, 102 aa, 1 stop
><MW: 11382, pI: 8.72, NX(S/T): 0
MTSSPLPRLLCSLVFLGGCWVTGFSSSLMWASAKEQLQHLFLIGSCLYKYFLPICHIASL
PPCLPWSTAESVSVPGMHTWTLSFPNRLSAGQHFVMFGCYRH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

N-myristoylation site:

Amino acids 18-24

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 9-20;36-47;

89-100

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FIGURE 55

ACACTGGCCAAACACTCGCATCCAGGGCGTCTCCGGCTGCTCCCATTGAGCTGTCTGCTCG
CTGTGCCCCGCTGTGCCTGCTGTGCCCCGCGCTGTCGCCGCTGCTACCGCGTCTGCTGGACGCG
GGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCG
AGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTC
CTGGGTGGTGTCATCCCCTTGGGGCTGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCT
GCCCAACGTCACTCTCTTAGAGGAGCTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCC
GGGTCCGCAGAGCCATCCCCAGGGAGGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTT
CGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACATGACCTGGGATGACGAACTGGA
GAAGTCTGCTGCAGCGTGGGCCAGTCAGTGCATCTGGGAGCACGGGGCCACCAGTCTGCTGG
TGTCCATCGGGCAGAACCTGGGCGCTCACTGGGGCAGGTATCGCTCTCCGGGGTTCCATGTG
CAGTCTTGGTATGACGAGGTGAAGGACTACACCTACCCCTACCCGAGCGAGTGC AACCCCTG
GTGTCCAGAGAGGTGCTCGGGGCCTATGTGCACGCACTACACACAGATAGTTTGGGCCACCA
CCAACAAGATCGGTTGTGCTGTGAACACCTGCCGGAAGATGACTGTCTGGGGAGAAGTTTGG
GAGAACGCGGTCTACTTTGTCTGCAATTATTCTCCAAAGGGGAAGTGGATTGGAGAAGCCCC
CTACAAGAATGGCCGGCCCTGCTCTGAGTGCCCAACCAGCTATGGAGGCAGCTGCAGGAACA
ACTTGTGTTACCGAGAAGAAACCTACACTCCAAAACCTGAAACGGACGAGATGAATGAGGTG
GAAACGGCTCCCATTCCTGAAGAAAACCATGTTTGGCTCCAACCGAGGGTGATGAGACCCAC
CAAGCCCAAGAAAACCTCTGCGGTCAACTACATGACCCAAGTCGTCAGATGTGACACCAAGA
TGAAGGACAGGTGCAAAGGGTCCACGTGTAACAGGTACCAGTGCCAGCAGGCTGCCTGAAC
CACAAGGCGAAGATCTTTGGAAGTCTGTTCTATGAAAGCTCGTCTAGCATATGCCGCGCCGC
CATCCACTACGGGATCCTGGATGACAAGGGAGGCCTGGTGGATATCACCAGGAACGGGAAGG
TCCCCTTCTTCGTGAAGTCTGAGAGACACGGCGTGCACTCCCTCAGCAAATACAAACCTTCC
AGCTCATTCATGGTGTCAAAAGTGAAAGTGCAGGATTTGGACTGCTACACGACCGTTGCTCA
GCTGTGCCCGTTTGAAAAGCCAGCAACTCACTGCCCAAGAATCCATTGTCCGGCACACTGCA
AAGACGAACCTTCCTACTGGGCTCCGGTGTGTTGGAACCAACATCTATGCAGATACCTCAAGC
ATCTGCAAGACAGCTGTGCACGCGGGAGTCATCAGCAACGAGAGTGGGGGTGACGTGGACGT
GATGCCCGTGGATAAAAAGAAGACCTACGTGGGCTCGCTCAGGAATGGAGTTCAGTCTGAAA
GCCTGGGGACTCCTCGGGATGGAAAGGCCTTCGGGATCTTGCTGTGTCAGGCAG**TGA**ATTTC
AGCACCAGGGGAGAAGGGGCGTCTTCAGGAGGGCTTCGGGGTTTTGCTTTTATTTTATTTT
GTCATTGCGGGGTATATGGAGAGTCA

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FIGURE 56

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131590
><subunit 1 of 1, 497 aa, 1 stop
><MW: 55906, pI: 8.43, NX(S/T): 4
MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEIL
MLHNKLRGQVQPQASNMHEYMTWDDELEKSAAAWASQCIWEHGPTSLLVSIGQNLGAHWGR
YRSPGFHVQSWYDEVKDYTYPPSECNPWCPERC SGPMCTHYTQIVWATTNKIGCAVNTC
RKMTVWGEVWENAVYFVCNYS PKGNWIGEAPYKNGRPCSECP PSYGGSCRNNLCYREETY
TPKPETDEMNEVETAPIPEENHVWLQPRVMRPTKPKKTS AVNYMTQVVRCDTKMKDRCKG
STCNRYQCPAGCLNHKAKIFGSLFYESSSSICRAAIHYGILDDKGGLVDITRNGKVPFFV
KSERHGVQSLSKYKPSSSFMVSKVKVQDLDCYTTVAQLCPFEKPATHCPRIHCPAHCKDE
PSYWAPVFGTNIYADTSSICKTAVHAGVISNESGGDVDVMPVDKKKTYVGS LRNGVQSES
LGTPRDGKAFRIFAVRQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 27-31;41-45;451-455

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 181-185;276-280;464-468

Tyrosine kinase phosphorylation site:

Amino acids 385-393

N-myristoylation sites:Amino acids 111-117;115-121;174-180;204-210;227-233;300-306;
447-453;470-476**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

Amino acids 195-207

SCP-like extracellular protein:

Amino acids 56-208

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FIGURE 57

GCACGAGGCCAAACACAGCAGCCTCAACATGAAGGTGGTTATGGTCCTCCTGCTTGCTGCCC
TCCCCCTTTACTGCTATGCAGGTTCTGGTTGCGTTCTTCTGGAGAGCGTCGTGGAAAAGACC
ATCGATCCATCGGTTTCTGTGGAGGAATACAAAGCAGATCTTCAGAGGTTTCATCGACACTGA
GCAAACCGAAGCAGCTGTAGAGGAGTTCAAGGAGTGCTTCCTCAGCCAGAGCAATGAGACTC
TGGCCAACTTCCGAGTCATGGTGCATACGATATATGACAGCCTTTACTGTGCTGCGTATTAA
CTGTCACAAGAACTTTGGCTCAGAGGAATCCAGACGATGCTCACAACCCGACTGTGGACTGG
CAGAAATCTCAACTTTTCCTTTTGACTTTCCCCTTTGATCAGTAATATGGAAGACGTTGTTG
AAACCTGAAGTATAGTTAATTTAAATAAACCCACTGCAAGAAAAAAAAAAAAA

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FIGURE 58

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA135173
><subunit 1 of 1, 93 aa, 1 stop
><MW: 10456, pI: 4.37, NX(S/T): 1
MKVVMVLLLAALPLYCYAGSGCVLLESVVEKTIDPSVSVEEYKADLQRFIDTEQTEAAVE
EFKECFLSQSNETLANFRVMVHTIYDSLYCAAY
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 12-23

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FIGURE 59A

CAAGTCCGTTGAGGCTGCCAGGCGAGTCAGGTCTCTCTGGACCTCGCCTGACTCGGCTGGGC
TGTGCCTGAAATTGACCCAGCTCCACCATACTCCTTGATT**ATG**GAGAAAACAAGGAGTAAGCT
CAAAGCGGCTGCAATCTTCCGGCCGCGAGCCAGTCTAAGGGGCGGCGCGGGGCTCCCTCGCC
CGGGAGCCGGAGGTAGAGGAGGAGGTGGAAAAGTCGGTCCTAGGCGGCGGGGAACTGCCAAG
GGGCGCCTGGAGGTCTCCCCGGGGAGGATCCAAAGTCTGAAAAGAGCGAAAAGGCTTGGAGC
TAGAGGTGGTGGCCAAGACCTTTCTTCTCGGCCCCCTTCCAGTTCGTCCGTAATTCCTGGCG
CAGCTCCGGGAAAAGGTGCAGGAAGTGCAGGCGCGGCGGTTCTCCAGCAGAACCCTCTCGG
CATCGCTGTCTTTGTGGCAATTTTACATTGGTTACATTTAGTAACACTTTTTGAAAATGATC
GTCATTTCTCTCACCTCTCATCTTTGGAACGGGAGATGACTTTTCGCACTGAAATGGGACTT
TATTATTCATACTTCAAGACCATTATTGAAGCACCTTCGTTTTTGGGAAGGACTGTGGATGAT
TATGAATGACAGGCTTACTGAATATCCTCTTATAATTAATGCAATAAAACGCTTCCATCTTT
ATCCAGAGGTAATCATAGCCTCCTGGTATTGCACATTCATGGGAATAATGAATTTATTTGGA
CTAGAACTAAGACCTGCTGGAATGTCACCAGAATAGAACCTCTTAATGAAGTTCAAAGCTG
TGAAGGATTGGGAGATCCTGCTTGCTTTTATGTTGGTGTAATCTTTATTTTAAATGGACTAA
TGATGGGATTGTTCTTCATGTATGGAGCATACCTGAGTGGGACTCAACTGGGAGGTCTTATT
ACAGTACTGTGCTTCTTTTCAACCATGGAGAGGCCACCCGTGTGATGTGGACACCACCTCT
CCGTGAAAGTTTTTTCCTATCCTTTCCCTTGACTTTCAGATGTGTATTTTAACTTTGATTCTCA
GGACCTCAAGCAATGATAGAAGGCCCTTCATGCACTCTGTCTTTCCAATGTTGCTTTTATG
CTTCCCTGGCAATTTGCTCAGTTTATACTTTTTTACACAGATAGCATCATTATTTCCCATGTA
TGTTGTGGGATACATTGAACCAAGCAAATTTTCAAGATCATTATATGAACATGATTTTCAGTT
ACCCTTAGTTTCATTTTGATGTTTGGAAATTCATGTACTTATCTTCTTATTATTCTTCATC
TTTGTTAATGACGTGGGCAATAATTCTAAAGAGAAATGAAATTCAAAACTGGGAGTATCTA
AACTCAACTTTTGGCTAATTCAAGGTAGTGCTGGTGGTGTGGAACAATCATTTTGAAATTT
CTGACATCTAAAATCTTAGGCGTTTCAGACCACATTGCGCTGAGTGATCTTATAGCAGCCAG
AATCTTAAGGTATACAGATTTTGATACTTTAATATATACCTGTGCTCCCGAATTTGACTTCA
TGGA AAAAGCGACTCCGCTGAGATACACAAAGACATTATTGCTTCCAGTTGTTATGGTGATT
ACATGTTTTATCTTTAAAAGACTGTTTCGTGATATTTTCATATGTTTTAGCTACAAACATTTA
TCTAAGAAAACAGCTCCTTGAACACAGTGAGCTGGCTTTTTCACACATTGCAGTTGTTAGTGT
TTACTGCCCTTGCCATTTTAAATTATGAGGCTAAAGATGTTTTTGACACCGCACATGTGTGTT
ATGGCTTCCTTGATATGCTCTCGACAGCTCTTTGGCTGGCTTTTTCGCAGAGTTCGTTTTGA
GAAGGTTATCTTTGGCATTTTAAACAGTGATGTCAATACAAGGTTATGCAAACCTCCGTAATC
AATGGAGCATAATAGGAGAATTTAATAATTTGCCTCAGGAAGAACTTTTACAGTGGATCAAA
TACAGTACCACATCAGATGCTGTCTTTCAGAGTGCCATGCCTACAATGGCAAGCATCAAGCT
GTCTACACTTCATCCCATTGTGAATCATCCACATTACGAAGATGCAGACTTGAGGGCTCGGA
CAAAAATAGTTTATTCTACATATAGTCGAAAAATCTGCCAAAGAAGTAAGAGATAAATTGTTG
GAGTTACATGTGAATTATTATGTTTTAGAAGAGGCATGGTGTGTTGTGAGAACTAAGCCTGG
TTGCAGTATGCTTGAAATCTGGGATGTGGAAGACCCTTCCAATGCAGCTAACCCTCCCTTAT
GTAGCGTCCTGCTCGAAGACGCCAGGCCTTACTTCACCACAGTATTTTCAAGATAGTGTGTAC
AGAGTATTAAAGGTTAACT**TGA**GGAAGGATACTACCCATTTTACTATGGCACAAATGCCGTGTGT
CAAAAACAATCACCCCTTTGGCTTATTCACATTAATAAAAATCACAAAGCTTTAATAACAGACA
CTTAAAAATAAGATAAAAATGGATTGGAAATTTTTCTGATTACTAAAAGGTAAATTACTTTT
CTGTTCAATTGAATGTCAGCCTTATTAAGCTTGTCAATAAAGTTATTAAATCATTCATGTCAT
ACTGCATAAACAAATGTTCAATTCAGAATTTTAAAGAGAAATGTATATAAAGAACMATGATT
TTAATAATCAGGGGTATGTAAGTCCTTTTTCATCCAAGTGAATTGCTTCAGATTTTCT
CTAGTACCAGAGGGTACCTCCTCAAACCTTTTGAACCACTTAAGGCAGAAGAAATGCAAGCTC
TGAAATGACATCCTTAAAATGCTGATACTGGTCACAGCCTCTTTACCTCTGTGAGGAAATTG
TAACAGTGTGTCTTTTAAAGGTGTTTTATTTTACCAGCCCTTAAGAAAGATCTCTAATACCT
TTTTAATACTTTTTTTTAAATAATTTCAAGTTGAAGTGTTTTTAAAACACTTGTTTTGTAAAT
GTTTTGAATCTCTTGAGATGTGTTTACCCCACTAGATACATATTTGCCACTGGTTAGTTCTC
CATCTAAGCTCAAGAGGTTATTCATCTCTCTTAGATTCCAGTGGCTTTTCTTTTAAACATCC
AGGTA AAAACAGAACTGCTATGGTATACAACCAAGTTTTTGGGGTTAAACATAATCAGAAAAG

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FIGURE 59B

AAAATCCAGTTAAATTTATGAAGTGAGATTTTCAGATCCTAGATCTTGAATAAAGGAAAGGT
CTTTTCATCTTGATGGCCCCAAAGCTTGTTGGTCATGGTCTTTATTTCTGGCCACTATCTTC
TTAAATAATATATTTTTAAGCCCTCATTATTTTTGGTTTTGGGTGAGGAAAGTCATGTTTT
CTAAGTCCTCTCCCCTAATAAAACCTACCCAACAATAGTGCTTTGAAAAGTGGTAGTTATCT
TGAAGATACTCTTGCCAAATGCAAAGATAAACATTCTTTTTGTCTGCTTTATAAATATGAAA
TATGCCAGATCTATAGTATTTAATGTGCATCTACTTTAAATGAGTCATCTTGGGGTTTTTA
TAATTCCTTATGTTCTTGCCCCCTACACTTGAAATAACAAAATGCCTTAATTTTATGGAT
TAGTTCTCTTATAGTAGACAGGCAGCTATATGCAGCAAAACCAATAAAGTTATTTTCAACT
TTCATAGTTGTAAATATCTTATAACCAGAATACAAAACAGCTAAGAAAACATGCCACATTTTAT
TTTAGCATTTTCAAATAATTTGTTTTTGGTGTAGCACAGGATAAAAAAGGAGAGCGTCAAA
GAAAAGAGACATAACACCTAACATTCATAAAAATTAACAAAGTATATTTTGGATGATGTTTT
TACAGGAAATATTTTAAATAAGTTGGTAGAACTTTTAAAATGGTACTGTATTAGCTAATAAA
ATATTCAGTACAAATATATGTTTGGATTTATGCATTAAAAAACTAATAAAATTATTTCCAAC
TTTA

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FIGURE 60

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA138039
><subunit 1 of 1, 758 aa, 1 stop
><MW: 87354, pI: 9.36, NX(S/T): 1
MRKQGVSSKRLQSSGRSQSKGRRGASLAREPEVEEEVEKSVLGGGKLPRGAWRSSPGRIQ
SLKERKGLELEVAKTFLLGPFQFVRNSLAQLREKVQELQARRFSSRTTLGIAVFVAILH
WLHLVTLFENDRHFSHLSSLEREMTFRTMGLYYSYFKTIEAPSFLEGLWMIMNDRLTE
YPLIINAIKRFLYPEVIIASWYCTFMGIMNLFGLETKTCWNVTRIEPLNEVQSCEGLGD
PACFYVGVI FILNGLMMGLFFMYGAYLSGTQLGGLITVLCFFFNHGEATRVMTPLRES
FSYPFLVLQMCILTILIRTSSNDRPFIALCLSNVAFMLPWQFAQFILFTQIASLFPMYV
VGYIEPSKFQKIIYMNMISSVTLSFILMFGNSMYLSSYYSSLLMTWAIILKRNEIQKLG
SKLNFELIQGSAWWCGTIIILKFLT SKILGVSDHIRLSDLIAARILRYTDFDTLIYTCAPE
FDFMEKATPLRYTKTLLLPVVMVITCFIFKKTVRDISYVLATNIYLRKQLEHSELAFT
LQLLVFTALAILIMRLKMFLT PHMCVMASLICSRQLFGWLFRRVRFEKVIFGILTVMSIQ
GYANLRNQWSIIGEFNNLPQEELLQWIKYSTTSDAVFAGAMPTMASIKLSTLHPIVNHPH
YEDADLRARTKIVYSTYSRKSAREVRDKLLELHVNYVLEEAWCVVRTKPGCSMLEIWDV
EDPSNAANPPLCSVLLEDARPYFTTVFQNSVYRVLKVN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 109-124;197-213;241-260;266-283;302-315;336-356;
376-391;430-450;495-509;541-560;584-599;634-647

N-glycosylation site:

Amino acids 222-226

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 102-106

Tyrosine kinase phosphorylation site:

Amino acids 511-519

N-myristoylation sites:

Amino acids 24-30;50-56;151-157;254-260;264-270;269-275;
273-279;639-645

Amidation site:

Amino acids 20-24

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FIGURE 61

GGCGCGGCCACATCCTTTAAATATGGTCTTTCTTGGGCGCGCGGACAATGTGAGGAGTGGG
GTGGAGCGTGTGTGGTGTGTGGCTGCGGCCTGGGCAAGAGCCGCCGCGGACCATGAGCTGAG
TAAGTTCTGGAGGGATCCTGCCTCTTGGAGCCTTCGCAGCCAGGCAGCTGTGAACTGTGAGC
TAGAGTGAAGCAGAAATCTAGGAAGATGAGCTCCAAGATGGTCATAAGTGAACCAGGACTGA
ATTGGGATATTTCCCCCAAAAATGGCCTTAAGACATTTTCTCTCGAGAAAATTATAAAGAT
CATTCCATGGCTCCAAGTTTAAAAGAAGTACGTGTTTTATCCAACAGACGTATAGGAGAAAA
TTTGAATGCCTCAGCAAGTTCTGTAGAAAATGAGCCGGCAGTTAGTTCAGCAACTCAAGCAA
AGGAAAAAGTTAAAACCACAATTGGAATGGTTCTTCTTCCAAAACCAAGAGTTCCTTATCCT
CGTTTCTCTCGTTTCTCACAGAGAGAGCAGAGGAGTTATGTGGACTTGTTGGTTAAATACGC
AAAGATTCCTGCAAATTCCAAAGCTGTTGGAATAAATAAAAATGACTACTTGCGAGTACTTGG
ATATGAAAAACATGTGAACGAAGAAGTTACTGAGTTCCTAAAGTTTTTGCAGAATTCTGCA
AAGAAATGTGCGCAGGATTATAATATGCTTTCTGATGATGCCCGTCTCTTCACAGAGAAAAT
TTTAAGAGCTTGCATTGAACAAGTGAAAAAGTATTCAGAATTCTATACTCTCCACGAGGTCA
CCAGCTTAATGGGATTCTTCCCATTCAGAGTAGAGATGGGATTAAAGTTAGAAAAAACTCTT
CTCGCATTGGGCAGTGTAATAATGTGAAAACAGTATTTCCCTCAATGCCTATAAAGTTGCAG
CTGTCAAAGGACGATATAGCTACCATTTGAAACGTGAGAACAACAGCTGAAGCTATGCATTA
TGATATTAGTAAGATCCAAATGCAGAGAAGCTTGTTCAGATATCACCTCATAGTAGCTC
TAAGTGTGAGTCAATTTTACCTTATTAAATAATCATGGACCAACGTACAAGGAACAGTGG
GAAATTCAGTGTGTATTCAAGTAATACCTGTTGCAGGTTCAAAACCAGTTAAAGTAATATA
TATTAATTCACCACTTCCCCAAAAGAAAATGACTATGAGAGAGAGAAATCAAATCTTTCATG
AAGTTCATTAAAAATTTATGATGTCCAAAACACATCTGTTCCAGTCTCTGCAGTCTTTATG
GACAAACCTGAAGAGTTTATATCTGAAATGGACATGTCCTGTGAAGTCAACGAGTGCCGAAA
AATTGAGAGTCTTGAAAACCTTGATTTTGGATTTTGTGATGATGTCACAGAAGTGAACCTT
TTGGAGTAACCAACCAAGTATCAAAATCACCAAGTCCAGCAAGTACTTCCACAGTACCT
AACATGACAGATGCTCCTACAGCCCCCAAGCAGGAAGTACAAGTGTGGCACCAAGTGCACC
AGACATTTCTGCTAATTCTAGAAGTTTATCTCAGATTCTGATGGAACAATTGCAAAAGGAGA
AACAGCTGGTCACTGGTATGGATGGTGGCCCTGAGGAATGCAAAAATAAAGATGATCAGGGA
TTTGAATCATGTGAAAAGGTATCAAATCTGACAAGCCTTTGATACAAGATAGTGAAGTGA
AACATCTGATGCCTTACAGTTAGAAAATTCTCAGGAAATTGAACTTCTAATAAAAATGATA
TGACTATAGATATACTACATGCTGATGGTGAAAGACCTAATGTTCTAGAAAACCTAGACAAC
TCAAAGGAAAAGACTGTTGGATCAGAAGCAGCAAAAAGTGAAGATACAGTTCTCTGCAGCAG
TGATACAGATGAGGAGTGTTTAATCATTGATACAGAATGTAAAAAAACCAGTTATAACAGTG
TTTAAATTTAGATAAGTTTGGGGAAAATAATCAGTAGGCAAGAGGAACATTTTTCCTGTAGT
AGCTAGAGTGCCTTGAAAAATGTGTTGGCTATGTGAAGGAATATTTCAACTAAAATGGAAT
GGTATGCTTTTCAACCCTTAAAGTTTGGAGGAGGATCTTGATATGTTTTAACATTATCATGGCA
GGGAAATATATAAAGAAGAAAAATATTTTACATTAAACCTTTTCTAAAAATGTAAATAGA
AAAATAATTTGGTTTTTTTATCAAGAACAACACTTATCGTTATGTATTGTGTTAGTTATATTG
CCAGTCTGTTGCGACTGACTCAAAAAGTTAAATGTTGCCACTGCTGAAGATGATTATGAGCA
TCGCAAACCTTTGTTTCTGACCCATTTTGACAGTTTTTATATACTCCTTTAAATGATGAATG
TTACAGGTTAATAAAGTTAATACCTTTAA

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FIGURE 62

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139540
><subunit 1 of 1, 592 aa, 1 stop
><MW: 66453, pI: 5.42, NX(S/T): 3
MSSKMVISEPGLNWDISPKNGLKTFFSRENYKDHSMAPSLKELRVLSNRRIGENLNASAS
SVENEPAVSSATQAKEKVKTIGMVLLPKPRVPYPFRFSRFSQREQRSYVDLLVKYAKIPA
NSKAVGINKNDYLQYLDMMKKHVNEEVTEFLKFLQNSAKKCAQDYNMLSDDARLFTEKILR
ACIEQVKKYSEFYTLHEVTSLMGFFPFRVEMGLKLEKTLALGSKYVKTVPFSPMPIKLQ
LSKDDIATITETSEQTAEAMHYDISKDPNAEKLVSRYHPQIALTSQSLFTLLNHHGPTYKE
QWEIPVCIQVIPVAGSKPVKVIYINSPLPQKKMTMRERNQIFHEVPLKFMMSKNTSVPVS
AVFMDKPFEFISEMDMSCEVNECRKIESLENLYLDFDDDVTELETFGVTTTKVSKSPSPA
STSTVPNMTDAPTAPKAGTTTVAPSAPDISANSRSLSQILMEQLQKEKQLVTGMDGGPEE
CKNKDDQGFESCEKVSNSDKPLIQDSLKTS DALQLENSQEIETSNKNDMTIDILHADGE
RPNVLENLDNSKEKTVGSEAAKTEDTVLCSSDTDEECLIIDTECKKTSYNSV
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 56-60;354-358;427-431

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 187-191;331-335;585-589

N-myristoylation sites:

Amino acids 126-132;407-413;557-563

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FIGURE 63

TTTTTAACTTGAACTTCCAAGGCCACGTGCGTCTCCTGGCTCCTGCACGGACTGTGTGACTG
TCCCCGACAGCTTTCCTGTCTCGTCTCATGAGGGGTCCAGCACATGGCATTCTGGGTCTGGCA
CCTGAAGTCCACCTCTATGAGACCCTCTGGGAGCGTGACGGGGCCTTGGC**AT**GGGTCTGGCCG
AGGCCCTTCTGTCCCAGGTCACTGGTGTGGTCGGCCCCAGGCCCTCCTGTCCCACATCACCTG
TGTGGTCTGGCCCCAGGCCCTCCTGTCCCAGGTCAACGGTGTGGTCGGCCCCAGGCCCTCCTGTG
CAGGTCTCCTGTCCAGGTCACTGGTGTGGTCGGCCCCAGGCCCTTCTGTCCCAGGTCACTG
TGTGGTCTGGCCCCAGGGCCCTCCTGTACCATGTCACTGTTGAGGGGTGGCTCTGGAAGAGGG
CAGGGACTTGGCATTGGTGGGGGCAGGGTCCAAAGGTGTGGCCTGTGAGCAGGAAGGGGCAG
GTGGCATGGGTCCAGGCGGGACTCAGGGCTGGGGTGCCACTGCTGGAGACTGTCCGGAGGCC
CCTCCAGGGCACCTTGCCATTGCCATTGTGCTCATGGCCATCTGGTCCCGTTTCAGGGAAC
AAGAGGAGGATCAGATGCTGCGGGACATGAT**TG**AGAAGCTGGGTGACTGGGCCGGGGATGCT
GAGGGCTGGGCTGGCTGGCTGGGTGGGCCGGGGATGCTGAGTGTGGGCTGGCTGGCTGGGT
GGACCGGGCCTCCAGCTGGGGGTGGGGGGGGGGCGGGTATCGGGTCCCCCCTCAGCCTTGG
TGACAGGACAGGCAGGTTCACCCTGAGGGTGAGAGCTCCCTCCCGCCCCTAAGAGAGCCAGG
GGCAGCTGGTGACCGTGTGGTCATGGTGGGGACAGCCCTCCGGGGCACCCAGTCTGGGGCAG
GTTCTCACGTGGGAGGGCACAGGGCTTCTGTCAGGCTCGGAGGCCAGGGCGGATTGTGGCC
AGTGGAAGGGAAGGATGTTTCTGGCAGGGGGACTTGTGTGGGCCACGGCTGTGCGGCTGCGG
CGTTGAGCACGGCCTCACTGTCCACCTGTCCCCTAGGCCTCCAGAGGAAGAAGTCCAAGTTC
CGCTTGTCCAAGATCTGGTCACCAAAAAGCAAAAGCAGCCCCTCCCAGTAGTAGCCAGTAGG
GCCGTGGGCTCGGCCCCGACCTGGCATCCGGACTTGGACTCGGGGCCATGGGCTTGGCCCCG
ACCCGGAACCCGGAATTGTACTCGGGGCCGTGGGCTCGGCCCGGACCCGGCATTCTGGACTTG
GACTCGGGAAGGGCCTCCTGTCCCTACAAGGGGCATGTGGACAGCAGGGACCTGCGCTACCG
TCTGTGGTCTCAATAAAGAAACCGACCACATGGCCCCGGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAACA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139602
><subunit 1 of 1, 159 aa, 1 stop
><MW: 15900, pI: 8.07, NX(S/T): 0
MGRPRPFCPRSLVWSAQALLSHITCVVGP GPPVPGHRCGRPRPSCPGPPVQVTGVVGP GP
SVPGHLCGRPRALLYHVTVEGLALEEGRDLALVGAGFQGVACQQEGAGGMGPGGTQGWGA
TAGDCPEAPPGH LAIAIVAHGHLVPFQGTRGGSDAAGHD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

N-myristoylation sites:

Amino acids 109-115;113-119;119-125;148-154;151-157;152-158

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FIGURE 65

GGCGACCACCGCCGCCTCCTCACCTGGCCATTGGTGCAGCCCGTTCCCGGCGGCGAGAGAAG
GCAGGCGCGCTCCTTGCGCCACGCCACACCGTCGGGCCCCCGTCGGGTCCCCCTCGGGCCGCA
ATGGTGGGCTCCGCGCGGCTGGGTCCGGCACTCTTGACCCCCCTTTGTAACCACCGCGGCGGG
CACCCAGGGAGTTCGAGCAACGAAGTTGGTGACCTGCCCCGCTCCCAGGCAGTTTGCTGTTG
GGGCTTTCACGGCTGCTGGAAGGGCATGGCTGTTTGTCCCATCACTGGGCGCCAGCTTCTCA
AAGCTACGTTACAGCAACGCAGTAGGGACTTTCGTGGCAGGCTTTTTTTAAGAGCTGAAAG
AAGGGCGGGAGGGTTTACGTCC**TAG**GGTGATGATTTCCCTCACCAGACAGCGAAGTATCTATT
GGGAAACTCCAGGTGACCGCACCTCCTTCCGACAGTTCGCCCCGGGGCAAGTTTACCAGCTG
CGTCAGAAAGCAGGTTTGCAAAATCCTTGGAGAACGGCCTGAGCTAAGGACTGGGGTCAGGA
GGGTTTTAAACTCATTCTGATTTTCTTGCAATCATATCTCTTGAAAGTTTTTATATTTTCCC
CAATATTTTTCTGAGTTGCTATATCCAATGAAAACAATGCTGATGTAGAGGTCCACCAGCCA
ATGCTTTATTGGAAGTCAACGAATGAGACCGAGGGTGGCCCATAATCAATCTCGGCACGCGG
GAATGTGAACCTCTTCCAAGGTCTGGGCGAGTCCCTAGAGTTACGCAGATGAAGGACATTGG
CCCTCGAGAATCTCACACCAGCAAAGAAGAGCACAAACGAAGCGCAAACACTACTTATGATCATT
GTGGCTTTGGGCAAGTTGTTGTAGCTCCCAGCAACAATTTCTTCACCTGGAGTGCAGCAATA
AATGATACTGGTGCTGCAGGGCAGCTAATAAGCTTCTGAATAATATATGCAAAGTACTTGGC
ACCATGAGCAGAACTCAGTATACCGTCACTGAAGAAATAGCTTATTTAATGATTACACTTTT
CATATGTGCAAGTAAAAGTTTGACTTTTAGGGAGAGCCTCACCTACGGAATGTCTTTTTTTAA
ATTTCTTTTTTAATTATACTTTAAGTTCTGGGATACATGTGCAGAACGTGCAGGTTTGTAC
ACAGGTATACATGTGCCATGGTGGTTTGCAGCACCCATCAACCCTTCATCTAGGTTTTTAAGC
TCCGCATGCATTAGTTATTTGTCCTAATGCTCTCCCTCCCCTTGTCCCCCACCCECAACAG
GCCTCAGGGTGTGATGTTCCCTCCCTGGGTCCATATGTTCTCATTGTTCAACTCCCACTTA
TGATGAGAACATGCAGTGTGTTGTTTTCTGTTCTGTGTTAGTTTGCTGAGAATGATGGTTT
CCAGCATCATCCACGTCCCTGCAAAGGACATGAATTCATTCTTTTTTATGGCTGCATGGTAT
TCCATGGTGTATATGTGCCACATTTTCTTCATCCAGTCTATCATTGATGGGCACCTGGGTTG
GTTCCAAGACTTTGTTATTGTGAACAGTGCTGCAATAAACATACGTTTGTATGTGTCAAAAA
AAAAAAAAAAAAAAAA

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FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139632
><subunit 1 of 1, 90 aa, 1 stop
><MW: 9586, pI: 12.18, NX(S/T): 0
MVGSARLGPALLTPFVTTAAGTQGVRA TKLVTC PAPRQFAVGAF TAAGRAWLFVPSLGAS
FSKLRSQQRSRDFRGRLFLRAERRAGGFTS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-myristoylation sites:

Amino acids 24-30;42-48;58-64

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FIGURE 67

CATGTCTAGACTGGGAGCCCTGGGTGGTGCCCGTGCCGGGCTGGGACTGTTGCTGGGTACCG
CCGCCGGCCTTGGATTCTGTGCCTCCTTTACAGCCAGCGATGGAAACGGACCCAGCGTCAT
GGCCGCAGCCAGAGCCTGCCCCAACTCCCTGGACTATACGCAGACTTCAGATCCCGGACGCCA
CGTGATGCTCCTGCGGGCTGTCCAGGTGGGGCTGGAGATGCCTCAGTGCTGCCAGCCTTC
CACGGGAAGGACAGGAGAAGGTGCTGGACCGCCTGGACTTTGTGCTGACCAGCCTTGTGGCG
CTGCGGCGGGAGGTGGAGGAGCTGAGAAGCAGCCTGCGAGGCCTTGCAGGGGAGATTGTTGG
GGAGGTCCGATGCCACATGGAAGAGAACCAGAGAGTGGCTCGGCGGCGAAGGTTTCCGTTTG
TCCGGGAGAGGAGTGACTCCACTGGCTCCAGCTCTGTCTACTTCACGGCCTCCTCGGGAGCC
ACGTTACAGATGCTGAGAGTGAAGGGGGTTACACAACAGCCAATGCGGAGTCTGACAATGA
GCGGGACTCTGACAAAGAAAGTGAGGACGGGGAAGATGAAGTGAGCTGTGAGACTGTGAAGA
TGGGGAGAAAGGATTCTCTTGACTTGGAGGAAGAGGCAGCTTCAGGTGCCTCCAGTGCCTTG
GAGGCTCCGAGGTTCCCTCAGGCTTGAGGATGTGCTGCCCCCTCCTGCAGCAGGCCGACGAGCT
GCACAGGGGTGATGAGCAAGGCAAGCGGGAGGGCTTCAGCTGCTGCTCAACAACAAGCTGG
TGTATGGAAGCCGGCAGGACTTCTCTGGCCCTGGCCCGAGCCTACAGTGACATGTGTGAG
CTCACTGAGGAGGTGAGCGAGAAGAAGTCATATGCCCTAGATGGAAAAGAAGAAGCAGAGGC
TGCTCTGGAGAAGGGGGATGAGAGTGCTGACTGTACCTGTGGTATGCGGTGCTTTGTGGTC
AGCTGGCTGAGCATGAGAGCATCCAGAGGCGCATCCAGAGTGGCTTTAGCTTCAAGGAGCAT
GTGGACAAAGCCATTGCTCTCCAGCCAGAAAAACCCATGGCTCACTTTCTTCTTGGCAGGTG
GTGCTATCAGGTCTCTCACCTGAGCTGGCTAGAAAAAAAAAACTGCTACAGCCTTGCTTGAAA
GCCCTCTCAGTGCCACTGTGGAAGATGCCCTCCAGAGCTTCCTAAAGGCTGAAGAACTACAG
CCAGGATTTTCCAAAGCAGGAAGGGTATATATTTCCAAGTGCTACAGAGAACTAGGGAAAAA
CTCTGAAGCTAGATGGTGGATGAAGTTGGCCCTGGAGCTGCCAGATGTCACGAAGGAGGATT
TGGCTATCCAGAAGGACCTGGAAGAACTGGAAGTCATTTTACGAGACT**TAA**CCACGTTTCACT
GGCCTTCATGACTTGATGCCACTATTTAAGGTGGGGGGCGGGGAGGCTTTTTTCTTCTAGAC
CTTGCTGAGATCAGGAAACCACACAAATCTGTCTCCTGGGTCTGACTGCTACCCACTACCAC
TCCCCATTAGTTAATTTATTCTAACCTCTAACCTAATCTAGAATTGGGGCAGTACTCATGGC
TTCCGTTTCTGTGTTCTCTCCCTTGAGTAATCTCTTAAAAAATCAAGATTCACACCTGCC
CCAGGATTACACATGGGTAGAGCCTGCAAGACCTGAGACCTTCCAATTGCTGGTGAGGTGGA
TGAAGTTCAAAGCTATAGGAACAAAGCACATAACTTGTCACTTTAATCTTTTTCACTGACTA
ATAGGACTCAGTACATATAGTCTTAAGATCATACCTTACCTACCAAGGTAAAAAGAGGGATCA
GAGTGGCCACAGACATTGCTTTCTTATCACCTATCATGTGAATTCTACCTGTATTCTGGG
CTGGACCACTTGATAACTTCCAGTGTCCTGGCAGCTTTTGGAAATGACAGCAGTGGTATGGG
TTTATGATGCTATAAAACAATGTCTGAAAAGTTGCCTAGAATATATTTTGTACAAACTTGA
AATAAACCAAATTTGATGTT

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FIGURE 68

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139686
><subunit 1 of 1, 470 aa, 1 stop
><MW: 52118, pI: 5.06, NX(S/T): 0
MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG
RHVMLLRVPPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG
EIVGEVRCHMEENQVRARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTAN
AESDNERDSKESEDGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGGSSGLEDVLP
LLQQADELHRGDEQGKREGFQLLLNKLVIYGSQDFLWRLARAYSMDCELTEEVSEKKS
ALDGKEEAEEALEKGDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQP
ENPMAHFLLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQSFLKAEELQPGFSKAG
RVYISKCYRELGKNSEARWWMKLALLELPDVTKEDLAIQKDLEELEVLIRD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 209-213

N-myristoylation sites:Amino acids 5-11;8-14;9-15;15-21;19-25;72-78;164-170;
174-180;222-228;230-236**Amidation sites:**

Amino acids 207-211;254-258

Cell attachment sequence:

Amino acids 250-253

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FIGURE 69

CCCACGCGTCCGAAACACTTTAAACCTGACCAGCTAAATGGATAAACCTAGCCTGCATAGCT
TTTAAACTGGGGTCTCATACAGCACAGGAGGCCTACTTGCTTCAAGAACTGAAAATCCAGAG
GATGAATTGCTTTATCTGGAATGGCAAAGCCAGCACATAAGGAATGCCAGTTTGTATGG
GGCTACTAGCTCACATGCGGGATCAGAATGGTGTGAATGACAGCCGCACTGTGTCTATGAAGG
TGGTGGTGGTTTCCGCACAAGAGACCAAATAAGAAGAAAGCTGAGAGAGGGGGGAAACGTTTTT
GGATGACAAAGGATGGGTTTCCATTTAATTACGCAGCTGAAAGGCATGAGTGTGGTGTGGT
GCTACTTCCTACACTGCTGCTTGTATGCTCACGGGTGCTCAGAGAGCTTGCCCCAAAGAACT
GCAGATGTGATGGCAAATTTGTGTACTGTGAGTCTCATGCTTTCGCAGATATCCCTGAGAAC
ATTTCTGGAGGGTCACAAGGCTTATCATTAAGGTTCAACAGCATTGAGAAGCTCAAATCCAA
TCAGTTTGCCGGCCTTAACCAGCTTATATGGCTTTATCTTGACCATAATTACATTAGCTCAGTG
GATGAAGATGCATTTCAAGGGATCCGTAGACTGAAAGAATTAATTCTAAGCTCCAACAAAAT
TACTTATCTGCACAATAAAACATTTACCCAGTTCCCAATCTCCGCAATCTGGACCTCTCCT
ACAATAAGCTTCAGACATTGCAATCTGAACAATTTAAAGGCCTTCGGAACTCATCATTTTG
CACTTGAGATCTAACTCACTAAAGACTGTGCCATAAGAGTTTTTCAAGACTGTGCGAATCT
TGATTTTTTGGATTTGGGTTACAATCGTCTTCGAAGCTTGTCGCGAAATGCATTTGCTGGCC
TCTTGAAGTTAAAGGAGCTCCACCTGGAGCACAAACAGTTTTTCCAAGATCAACTTGCTCAT
TTTCCACGTCTCTTCAACCTCCGCTCAATTTACTTACAATGGAACAGGATTTCGCTCCATTAG
CCAAGGTTTGACATGGACTTGGAGTTCCTTACACAACCTTGGATTTATCAGGGATGACATCC
AAGGAATTGAGCCGGGCACATTTAAATGCCTCCCCAATTTACAAAAATTGAATTTGGATTCC
AACAAGCTCACCAATATCTCACAGGAAACTGTCAATGCGTGGATATCATTAATATCCATCAC
ATTGTCTGAAAATATGTGGGAATGCAGTCGGAGCATTTGTCTTTATTTTTATTGGCTTAAGA
ATTTCAAAGGAAATAAGGAAAGCACCATGATATGTGCGGGACCTAAGCACATCCAGGGTGAA
AAGGTTAGTGATGCAGTGGAACATATAATATCTGTTCTGAAGTCCAGGTGGTCAACACAGA
AAGATCACACCTGGTGCCCCAAACTCCCCAGAAACCTCTGATTATCCCTAGACCTACCATCT
TCAAACCTGACGTCACCCAATCCACCTTTGAAACACCAAGCCCTTCCCCAGGGTTTCAGATT
CCTGGCGCAGAGCAAGAGTATGAGCATGTTTCATTTACAAAATTATTGCCGGGAGTGTGGC
TCTCTTTCTCTCAGTGGCCATGATCCTCTTGGTGATCTATGTGTCTTGGAACGCTACCCAG
CCAGCATGAAACAACCTCCAGCAACACTCTCTTATGAAGAGGCGGCGGAAAAAGGCCAGAGAG
TCTGAAAGACAAATGAATTCCCCTTTACAGGAGTATTATGTGGACTACAAGCCTACAACTC
TGAGACCATGGATATATCGGTTAATGGATCTGGGCCCTGCACATATACCATCTCTGGCTCCA
GGGAATGTGAGATGCCACACCACATGAAGCCCTTGCCATATTACAGCTATGACCAGCCTGTG
ATCGGGTACTGCCAGGCCCACCAGCCACTCCATGTCACCAAGGGCTATGAGACAGTGTCTCC
AGAGCAGGACGAAAGCCCCGGCCTGGAGCTGGGCCGAGACCACAGCTTCATCGCCACCATCG
CCAGGTCCGCAGCACCGGCCATCTACCTAGAGAGAATTGCAAACTAACGCTGAAGCCAACTC
CTCACTGGGGAGCTCCATGGGGGGGAGGGAGGGCCTTCATCTTAAAGGAGAATGGGTGTCCA
CAATCGCGCAATCGAGCAAGCTCATCGTTCTGTAAACATTTATGGCATAGGGAAAAAAA
AAAAAAAAAAAAA

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142392
><subunit 1 of 1, 590 aa, 1 stop
><MW: 67217, pI: 9.26, NX(S/T): 4
MGFHLITQLKGMSVVLVLLPTLLLVMLTGAQRACPKNCRCDGKIVYCESHAFADIPENIS
GGSQGLSLRFNSIQKLKSNQFAGLNQLIWLYLDHNYISSVDEDAFQGIRRLKELILSSNK
ITYLHNKTFHPVPNLRNLDLSYNKLQTLQSEQFKGLRKLIILHLRSNSLKTVPPIRVFQDC
RNLDFLDLGYNRLRSLSRNAFAGLLKLKELHLEHNQFSKINFAPRLENLRSIYLQWNR
IRSIQGLTWTWSSLHNLDLSGNDIQGIEPGTFKCLPNLQKLNLDNSNKLTNISQETVNAW
ISLISITLSGNMWECSRSICPLFYWLKNFKGNKESTMICAGPKHIQGEKVSDAVETYNIC
SEVQVVNTERSHLVPQTPQKPLIIPRPTIFKPDVTQSTFETPSPSPGFGQIPGAEQYEHV
SFHKIIAGSVALFLSVAMILLVIYVSWKRYPASMKQLQQHSLMKRRRKKARESERQMNSP
LQEYYVDYKPTNSETMDISVNGSGPCTYTTISGSRECEMPHHMKPLPYYSYDQPVIQYQA
HQPLHVTKGYETVSPEQDESPGLELGRDHSFIATARSAAPIYLERIAN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 425-443

N-glycosylation sites:

Amino acids 58-62;126-130;291-295;501-505

Tyrosine kinase phosphorylation site:

Amino acids 136-143

N-myristoylation sites:Amino acids 29-35;61-67;247-253;267-273;271-277;331-337;
502-508;512-518;562-568**Glycosyl hydrolases family:**

Amino acids 310-319

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FIGURE 71

TTCCAGTCAGAGTTAAGTTAAACAGAAAAAGGAAGATGGCAAGAATATTGTTACTTTTCC
TCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGAATATTTATGGACCGTCTAGCTTCCAAG
AAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTTCTCTGGCTAGTGCTCAAGAAGATTA
TAATGCCCCGGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGTGTACTCAA
AGCTGGTAAAAGAAAATGGAGCTGGAGAATTTGGGCTGGCAGTGTTTATGGTGATGGCCAG
GACGAGATGGGAGTCGTGGGTTATTTCCCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCA
GGAAGCTACCAAGGAAGTTCCCACCACGGATATTGACTTCTTCTGCGAGTAATAAATTAGTT
AAAAGCTCAAATAGAAAGAAAACACCAAAAATAAAGAAAAGAGCAAAAGTGGCCAAAAAATG
CATGTCTGTAATTTTGGACTGACGT

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143076
><subunit 1 of 1, 128 aa, 1 stop
><MW: 14332, pI: 4.83, NX(S/T): 0
MARILLLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTISLASAQEDYNAPDCRFINV
KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYPFRNLVKEQRVYQEATKEVPT
TDIDFFCE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-14

N-myristoylation site:

Amino acids 84-90

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FIGURE 73

CTCAGATTTGCCATGGAGAAATTTTCAGTCTCGGCAATCCTGCTTCTTGTGGCCATCTCTGG
TACTCTGGCCAAAGACACCCACAGTCAAATCTGGATCCAAAAAGGACCCAAAGGACTCTCGAC
CCAAACTACCCCAGACCCTGTCCAGAGGTTGGGGAGATCAGCTCATCTGGACTCAGACTTAC
GAAGAAGCCTTATACAAATCCAAGACAAGCAACAGACCCTTGATGGTCATTTCATCACTTGGA
CGAATGCCCCGACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAGGAGATCCAGAAATTG
GCAGAGCAGTTTGTTCCTCAACTTGATCTATGAAACAACGACAAGCACCTTTCTCCTGA
TGGCCAGTACGTCCCCAGAATTGTGTTTGTGGACCTTCCCTGACGGTGAGGGCAGACATCA
CCGGAAGATACTCAAACCGTCTCTACGCTTATGAACCTTCTGACACAGCTCTGTTGCACGAC
AACATGAAGAAAGCTCTCAAGTTGCTGAAGACAGAGTTGTAGAGTCAACTGTACAGTGCCTC
AGGAGCCGGGAAGGCAGAAGCACTGTGGACCTGCCGATGACATTACAGTTTAATGTTACAAC
AAATGTATTTTTTAAACACCCACGTGTGGGGAAACAATATTATTATCTACTACAGACACATG
ATTTTCTAGAAAATAAAGTCTTGTGAGAACTCCAAA

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FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143294
><subunit 1 of 1, 175 aa, 1 stop, 1 unknown
><MW: 19888.97, pI: 9.08, NX(S/T): 0
MEKFSVSAILLLVAISGTLAKDTTVKSGSKKDPKDSRPKLPQTL SRGWGDQLIWTQTYEE
ALYKSKTSNRPLMVIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLIYETTDKHLSP
DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALLHDNMKKALKLLKTEL
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

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FIGURE 75

GCCGGCGCCAGGGCAGGCGGGCGGCTGGCAGCTGTGGCGCCGAC**ATGGCT**GCGCTGGTGGAG
CCGCTGGGGCTGGAGCGGGACGTGTCCCGGGCGGTTGAGCTCCTCGAGCGGCTCCAGCGCAG
CGGGGAGCTGCCGCCGAGAAGCTGCAGGCCCTCCAGCGAGTTCTGCAGAGCCGCTTCTGCT
CCGCTATCCGAGAGGTGTATGAGCAGCTTTATGACACGCTGGACATCACCGGCAGCGCCGAG
ATCCGAGCCCATGCCACAGCCAAGGCCACAGTGGCTGCCTTCACAGCCAGCGAGGGCCACGC
ACATCCCAGGGTAGTGGAGCTACCCAAGACGGATGAGGGCCTAGGCTTCAACATCATGGGTG
GCAAAGAGCAAACTCGCCCATCTACATCTCCCGGGTCATCCAGGGGGTGTGGCTGACCGC
CATGGAGGCCTCAAGCGTGGGGATCAACTGTTGTCGGTGAACGGTGTGAGCGTTGAGGGTGA
GCAGCATGAGAAGGCGGTGGAGCTGCTGAAGGCGGCCAGGGCTCGGTGAAGCTGGTTGTCC
GTTACACACCGCGAGTGCTGGAGGAGATGGAGGCCCGGTTGAGAAGATGCGCTCTGCCCCG
CGGCGCCAACAGCATCAGAGCTACTCGTCCTTGGAGTCTCGAGGT**TGA**AACCACAGATCTGG
ACGTTACGTGCACTCTCTTCCTGTACAGTATTTATTGTTCTTGGCACTTTATTTAAAGATA
TTTGACCCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143514
><subunit 1 of 1, 207 aa, 1 stop
><MW: 22896, pI: 8.93, NX(S/T): 0
MAALVEPLGLERDVSRVAVELLERLQSRGELPPQKLQALQRVLQSRFCSAIREVYEQLYDT
LDITGSAEIRAHATAKATVAAFTASEGHAHPRVVVELPKTDEGLGFNIMGGKEQNSPIYIS
RVIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVLEE
MEARFEKMRSARRRQQHQSYSSLESRG
```

Tyrosine kinase phosphorylation site:

Amino acids 51-59

N-myristoylation sites:

Amino acids 102-108;133-139

Cell attachment sequence:

Amino acids 136-139

PDZ domain (Also known as DHR or GLGF):

Amino acids 93-174

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144841
><subunit 1 of 1, 208 aa, 1 stop
><MW: 22187, pI: 5.08, NX(S/T): 1
MDSDETGFEGHSLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHL
EIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC
SFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGIL
APQPPDVGSSDPLSMVGPSQGRSPSYAS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-myristoylation sites:

Amino acids 12-18;20-26;23-29;66-72;94-100;107-113;168-174

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 15-26

HBGF/FGF family proteins:

Amino acids 57-73;80-131

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FIGURE 79

AGTCCCAGACGGGCTTTTCCCAGAGAGCTAAAAGAGAAGGGCCAGAGAA**ATG**TCGTCCCAG
CCAGCAGGGAACCCAGACCTCCCCGGGGCCACAGAGGACTACTCCTATGGCAGCTGGTAC
ATCGATGAGCCCCAGGGGGGCGAGGAGCTCCAGCCAGAGGGGGAAGTGCCCTCCTGCCAC
ACCAGCATACCCCGGCCTGTACCACGCCTGCCTGGCCTCGCTGTCAATCCTTGTGCTG
CTGCTCCTGGCCATGCTGGTGAGGCGCCGCCAGCTCTGGCCTGACTGTGTGCGTGCCAGG
CCCCGGCCTGCCAGCCCTGTGGATTCTTGGCTGGGGACAGGCCCCGGGCAGTGCCCTGCT
GCTGTTTTTCATGGTCTCCTGAGCTCCCTGTGTTTGCTGCTCCCCGACGAGGACGCATTG
CCCTTCCTGACTCTCGCCTCAGCACCCAGCCAAGATGGGAAAAGTGAAGGCTCCAAGAGGG
GCCTGGAAGATACTGGGACTGTTCTATTATGCTGCCCTCTACTACCCTCTGGCTGCCTGT
GCCACGGCTGGCCACACAGCTGCACACCTGCTCGGCAGCACGCTGTCCTGGGCCCACCTT
GGGGTCCAGGTCTGGCAGAGGGCAGAGTGTCCCCAGGTGCCCAAGATCTACAAGTACTAC
TCCCTGCTGGCCTCCCTGCCTCTCCTGCTGGGCCTCGGATTCTCTGAGCCTTTGGTACCCT
GTGCAGCTGGTGAGAAGCTTCAGCCGTAGGACAGGAGCAGGCTCCAAGGGGCTGCAGAGC
AGCTACTCTGAGGAATATCTGAGGAACCTCCTTTCAGGAAGAAGCTGGGAAGCAGCTAC
CACACCTCCAAGCATGGCTTCCTGTCTGGGCCCGCGTCTGCTTGAGACACTGCATCTAC
ACTCCACAGCCAGGATTCCATCTCCCGCTGAAGCTGGTGTCTTCAGCTACACTGACAGGG
ACGGCCATTTACCAGGTGGCCCTGCTGCTGCTGGTGGGCGTGGTACCCACTATCCAGAAG
GTGAGGGCAGGGGTCACCACGGATGTCTCTACCTGCTGGCCGGCTTTGGAATCGTGCTC
TCCGAGGACAAGCAGGAGGTGGTGGAGCTGGTGAAGCACCATCTGTGGGCTCTGGAAGTG
TGCTACATCTCAGCCTTGGTCTTGTCTGCTTACTACCTTCCTGGTCTGTATGCGCTCA
CTGGTGACACACAGGACCAACCTTCGAGCTCTGCACCGAGGAGCTGCCCTGGACTTGAGT
CCCTTGCTATCGGAGTCCCCATCCCTCCCGCCAAGCCATATTCTGTTGGATGAGCTTCAGT
GCCTACCAGACAGCCTTTATCTGCCTTGGGCTCCTGGTGCAGCAGATCATCTTCTTCCTG
GGAACCACGGCCCTGGCCTTCCTGGTGTCTATGCCTGTGCTCCATGGCAGGAACCTCCTG
CTCTTCCGTTCCCTGGAGTCTCGTGGCCCTTCTGGCTGACTTTGGCCCTGGCTGTGATC
CTGCAGAACATGGCAGCCCATTGGGTCTTCTGGAGACTCATGATGGACACCCACAGCTG
ACCAACCGGCGAGTGCTCTATGCAGCCACCTTTCTTCTCTTCCCCCTCAATGTGCTGGTG
GGTGCCATGGTGGCCACCTGGCGAGTGCTCCTCTCTGCCCTCTACAACGCCATCCACCTT
GGCCAGATGGACCTCAGCCTGCTGCCACCGAGAGCCGCCACTCTCGACCCCGGCTACTAC
ACGTACCGAACTTCTTGAAGATTGAAGTCAGCCAGTCGCATCCAGCCATGACAGCCTTC
TGCTCCCTGCTCCTGCAAGCGCAGAGCCTCCTACCCAGGACCATGGCAGCCCCCAGGAC
AGCCTCAGACCAGGGGAGGAAGACGAAGGGATGCAGCTGCTACAGACAAAGGACTCCATG
GCCAAGGGAGCTAGGCCCGGGGCCAGCCGCGGCAGGGCTCGCTGGGGTCTGGCCTACACG
CTGCTGCACAACCCAACCTGCAGGTCTTCCGCAAGACGGCCCTGTTGGGTGCCAATGGT
GCCAGCCC**TGAG**GGCAGGGAAGGTCAACCCACCTGCCATCTGTGCTGAGGCATGTTCC
TGCTTACCATCCTCCTCCCTCCCCGGCTCTCCTCCCAGCATCACACCAGCCATGCAGCCA
GCAGGTCTCCGGATCACTGTGGTTGGGTGGAGGTCTGTCTGCACTGGGAGCCTCAGGAG
GGCTCTGCTCCACCCACTTGGCTATGGGAGAGCCAGCAGGGGTCTGGAGAAAAAACTG
GTGGGTTAGGGCCTTGGTCCAGGAGCCAGTTGAGCCAGGGCAGCCACATCCAGGCGTCTC
CCTACCCTGGCTCTGCCATCAGCCTTGAAGGGCCTCGATGAAGCCTTCTCTGGAACCACT
CCAGCCCAGCTCCACCTCAGCCTTGGCCTTCACGCTGTGGAAGCAGCCAAGGCACCTCCT
CACCCCTCAGCGCCACGGACCTCTCTGGGGAGTGGCCGGAAGCTCCCGGTCTCTGGC
CTGCAGGGCAGCCCAAGTCATGACTCAGACCAGGTCCCACACTGAGCTGCCCACACTCGA
GAGCCAGATATTTTGTAGTTTTTATGCCTTTGGCTATTATGAAAGAGGTTAGTGTGTTT
CCTGCAATAAACTTGTTCTGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 80**Protein File:**

MW: 73502.97, pI: 9.26

MSSQPAGNQTS PGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLS
ILVLLLLAMLVRRRQLWPDVCVRGRPGLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPD
EDALPFLT LASAPSQDGKTEAPRGAWKILGLFYAALYYPLAACATAGHTAAHLLGSTLS
WAHLGVQVWQRAECPQVPKIYKYSSLLASLPLLGLGLSLWYPVQLVRSFSRRTGAGSK
GLQSSYSEEYLRNLLCRKKLGSSYHTSKHGFLSWARVCLRHCIYTPQPGFHLPLKLVLSA
TLTGTAIYQVALLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKHHLW
ALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI FCW
MSFSAYQTAFICLGLLVQQIIFFLGTTALAFLVLMFVLHGRNLLFRSLESSWPFWLT LA
LAVILQNMAAHWVFLETHDGHQPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYN
AIHLGQMDLSLLPPRAATLDPGYYTYRNFLEKIEVSQSHPMATAFCSSLLQAQSLPRTMA
APQDSL RPGEEDEGMQLLQTKDSMAKGARPGASRGARWGLAYTLLHNPTLQVFRKTALL
GANGAQP

Important features of the protein:**Transmembrane domains:**

Amino acids 54-69;102-119;148-166;207-222;301-320;
364-380;431-451;474-489;512-531

N-glycosylation site:

Amino acids 8-12

N-myristoylation sites:

Amino acids 50-56;176-182;241-247;317-323;341-347;525-531;
627-633;631-637;640-646;661-667

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 364-375

ATP/GTP-binding site motif A (P-loop):

Amino acids 132-140

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FIGURE 81

AAAAAATACAGCAGGTGAAGGAGGTTGGAGAGTAGGGGGTGGAGGGGCCACGCAGCACTTGT
CCTTCACCCCTGGAGGGGATCTGTTACATGCCCCAGATTGCTGGTCCCCTAGAAATGTTACTG
AGGCAGCCTCTGCATTTTTGCAGGGATTGTTTTCTACTGTTTGACATTACGTAACCTCCTA
ACGCTGTCTGGGGAAGATGCTACCCCTGCTCTCCCCGTCTTTCCTGCACTCTCAGCAATGG
GATGGGCTGACTGATGCCCTGTGGGCTGGAAAGCTGACCACAGTTGCTGCAGACCAGACCCC
CTCACATAGTGAGTGCTGGGCTGAGGAATCCAGGAGAGCCCGAGGGGGGACACTGAAGGTGT
ATCGTTGGCCCTGCCAGCTGCAAGTGAAGTGTCTGATGAATTTTAATAGGGAGAAAGAAG
TATTTGCTAAGAATGGCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATC
AATATCCCATGAGGCTCATAAAACGAGTCTTCTTCTTGAAACATGACCAAGATTGGGCAA
ACGTCTCCAACATGACTTTCAGCAACGGAAACTAAGAGTCAAAGGCATTTATTACCGGAAT
GCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCT
ATGGTGTAATTTGAGGTCAGTGGCCAGAGGACAGATCCCGTCTACATTATGAGTGAAGCGGAGA
GCTACTGCAGGGTTCTGAGCAGAGTCCTAATTTATATTTTAGAAGAATCATCATGGCTCCTA
GATTAGGAATAAAACGAAGGGGGCCAGGGATGGAAACGATGAGTCCAGTTGGGTTACTGCAA
AGATCCAGGCCAGAAATCCAGGCACAGTGGCACACACCTGAGTCCCAGATAATTCCACCTAC
TGGTCCTGCTCTGTGGCCTACTGGTCCGAGTCCAGCCCCGACTGATTTCTGGGCCTGTAATG
TCTAAAAACGCTCCCTGCTGATGTTTTGCAAGTGAAGTGTGTTACTTGAAGGCAGTTCCTAGG
ATAAACTAGTCGCTTTATCATTACAGAATCATTCACTGAGCATCAACTATGTAACCAGCATT
GGGTTGGGTGCCAGAGATCCAAAGCTAAGACACCAAACCTGCTCTCCAGGAAACGAGAGGC
TGAGAA

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FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149995
><subunit 1 of 1, 95 aa, 1 stop
><MW: 10704, pI: 10.00, NX(S/T): 2
MAILTSLQLILLIPISISHEAHKTSLSWKHDQDWANVSNMFTSNGKLRVKGIYYRNAD
ICSRHRVTSAGLTQLDLQLWCNLRVARGQIPSTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

N-glycosylation sites:

Amino acids 38-42;41-45

N-myristoylation site:

Amino acids 89-95

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FIGURE 83

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCGGCTGACTGCGCCTCTGCTT
TCTTTCCATAACCTTTTCTTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTCGGA
CACTAGGGTGCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAACC**ATGCT**
GCCGCCGCCGCGGGCCGAGCTGCCTTGCGCTGCCTGTGCTCCTGCTACTGCTGGTGGTGC
TGACGCCGCCCCGACCGGCGCAAGGCCATCCCCAGGCCAGATTACCTGCGGCGCGGCTGG
ATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGAGTGCGCCGCGCC
GCGGGGCTGCCTGGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTGGGAATGCGCCAACC
TCGAGGGCCAGCTCTGCGACCTGGACCCCAGTGCTCACTTCTACGGGCACTGCGGCGAGCAG
CTTGAGTGCCGGCTGGACACAGGCGGCGACCTGAGCCGCGGAGAGGTGCCGGAACCTCTGTG
TGCCTGTCGTTTCGCAGAGTCCGCTCTGCGGGTCCGACGGTCACACCTACTCCAGATCTGCC
GCCTGCAGGAGGCGGCCCCGCGCTCGGCCCCGATGCCAACCTCACTGTGGCACACCCGGGGCCC
TGCGAATCGGGGCCCCAGATCGTGTCACATCCATATGACACTTGGAATGTGACAGGGCAGGA
TGTGATCTTTGGCTGTGAAGTGTTTGCCTACCCCATGGCCTCCATCGAGTGAGGAAGGATG
GCTTGGACATCCAGCTGCCAGGGGATGACCCCCACATCTCTGTGCAGTTTAGGGGTGGACCC
CAGAGGTTTGAAGTGACTGGCTGGCTGCAGATCCAGGCTGTGCGTCCCAGTGATGAGGGCAC
TTACCGCTGCCTTGGCCGCAATGCCCTGGGTCAAAGTGGAGGCCCTGCTAGCTTGACAGTGC
TCACACCTGACCAGCTGAACTCTACAGGCATCCCCCAGCTGCGATCACTAAACCTGGTTTCCT
GAGGAGGAGGCTGAGAGTGAAGAGAATGACGATTACTACT**AG**GTCCAGAGCTCTGGCCCATG
GGGGTGGGTGAGCGGCTATAGTGTTTCATCCCTGCTCTTGAAAAGACCTGGAAGGGGAGCAG
GGTCCCTTCATCGACTGCTTTTCATGCTGTCAGTAGGGATGATCATGGGAGGCCTATTTGACT
CCAAGGTAGCAGTGTTGGTAGGATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAG
ACCAGGACCGGTGGGGTACAAAGGGGGCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCA
ACAGGTTGTTTCCCAGGCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGAT
TCTCCACTTCTTCCAGCCCTGCTGGGCCACAGTTCTAACTGCCCTTCCTCCCAGGCCCTGGT
TCTTGCTATTTCCCTGGTCCCCAACGTTTATCTAGCTTGTTTGGCCTTTCCCCAACTCATCT
TCCAGAACTTTTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAACTGCAGTCCCTTTTGCT
GTCTGCCGTCTTTTGTACAAGAGAGAGAACAGCGGAGCATGACTTAGTTCAGTGCAGAGAGA
TTT

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FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA167678
><subunit 1 of 1, 304 aa, 1 stop
><MW: 32945, pI: 4.69, NX(S/T): 3
MLPPPRPAAALALPVLLLLLVLTTPPTGARPSGPDYLRRGWMRLLAEGEGCAPCRPEE
CAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRDGTGGDLRGE
VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHFGPCESGPQIVSHPYD
TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFVETGWLQI
QAVRPSDEGTYRCLGRNALQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN
DDYY
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 159-163;183-187;277-281

Tyrosine kinase phosphorylation site:

Amino acids 244-252

N-myristoylation sites:

Amino acids 52-58;66-72;113-119;249-255

Kazal-type serine protease inhibitor domain:

Amino acids 121-168

Immunoglobulin domain:

Amino acids 186-255

Insulin-like growth factor binding proteins:

Amino acids 53-90

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FIGURE 85

CAAAGCGCGGCTGTCCGCGGTGCCGGCTGGGGGCGGAGAGGCGGCGGTGGGCTCCCTGGGG
TGTGTGAGCCCGGT**GATG**GAGCCGGGCCCCGACAGCCGCGCAGCGGAGGTGTTCTGTTGCCGCC
GTGGCTGCCGCTGGGGCTGCTGCTGTGGTCGGGGCTGGCCCTGGGCGCGCTCCCCCTTCGGCA
GCAGTCCGCACAGGGTCTTCCACGACCTCCTGTGCGGAGCAGCAGTTGCTGGAGGTGGAGGAC
TTGTCCCTGTCCCTCCTGCAGGGTGGAGGGCTGGGGCCTCTGTGCTGCCCCGGACCTGCC
GGATCTGGATCCTGAGTGCCGGGAGCTCCTGTGGACTTCGCCAACAGCAGCGCAGAGCTGA
CAGGGTGTCTGGTGCGCAGCGCCCGGCCCGTGCGCCTCTGTGACACCTGCTACCCCTCTTC
CAACAGGTCGTCAGCAAGATGGACAACATCAGCCGAGCCGCGGGGAATACTTCAGAGAGTCAG
AGTTGTGCCAGAAGTCTCTTAATGGCAGATAGAATGCAAATAGTTGTGATTCTCTCAGAATT
TTTTAATACCACATGGCAGGAGGCAAATTGTGCAAATTGTTTAAACAAACAACAGTGAAGAAT
TATCAAACAGCACAGTATATTTCTTAATCTATTTAATCACACCCTGACCTGCTTTGAACAT
AACCTTCAGGGGAATGCACATAGTCTTTTACAGACAAAAAATTATTCAGAAGTATGCAAAAA
CTGCCGTGAAGCATACAAAACCTCTGAGTAGTCTGTACAGTGAAATGCAAAAAATGAATGAAC
TTGAGAATAAGGCTGAACCTGGAACACATTTATGCATTGATGTGGAAGATGCAATGAACATC
ACTCGAAAACATATGGAGTCGAACCTTCAACTGTTCACTCCCTTGCACTGACACAGTGCCTGT
AATTGCTGTTTCTGTGTTTCATTCTCTTTCTACCTGTTGTCTTCTACCTTAGTAGCTTTCTTC
ACTCAGAGCAAAAGAAACGCAAACCTCATTCTGCCCAAACGTCTCAAGTCCAGTACCAGTTTT
GCAAATATTCAGGAAAATTCAAAC**TGAG**ACCTACAAAATGGAGAATTGACATATCACGTGAA
TGAATGGTGGAAGACACAACCTTGGTTTCAGAAAGAAGATAAACTGTGATTTGACAAGTCAAG
CTCTTAAGAAATACAAGGACTTCAGATCCATTTTTTAAATAAGAATTTTCGATTTTTCTTTCC
TTTTCCACTTCTTTCTAACAGATTTGGATATTTTTTAATTTCCAG

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FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA168028
><subunit 1 of 1, 334 aa, 1 stop
><MW: 37257, pI: 5.95, NX(S/T): 10
MEPGPTAAQRRCSLPPWLPLGLLWSGLALGALPFGSSPHRVFHDLLSEQQLLEVEDLSL
SLLQGGGLGPLSLPPDLPLDPECRELLLDFASSAELTGCLVRSARPVRLCQTCYPLFQ
QVSKMDNISRAAGNTSESQSCARSLLMADRMQIVVILSEFFNTTWQEANCANCLTNSE
ELSNSTVYFLNLFNHTLTCTFEHNLQGNAHSLLOTKNYSEVCKNCREAYKTLSSLYSEMQK
MNELENKAEPGTHLCIDVEDAMNITRKLWSRTFNCSVPCSDTVPVIAVSVFILFLPVVFY
LSSFLHSEQKKRKLILPKRLKSSTSFANIQENSN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-31

Transmembrane domain:

Amino acids 278-300

N-glycosylation sites:Amino acids 93-97;128-132;135-139;163-167;177-181;
184-188;194-198;216-220;263-267;274-278**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 10-14

N-myristoylation sites:

Amino acids 27-33;206-212;251-257

Leucine zipper pattern:

Amino acids 190-212

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FIGURE 87

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCGCGGGCGCCCCAGGGC
GGGCAGGCGCCCCGCGCGGCCGCGGGGCTGCGCGGACCGGCCGGAGGAGCTACTGGAGCAGC
TGTACGGGCGCCTGGCGGCCGCGCTGCTCAGTGCCCTTCCACCACACGCTGCAGCTGGGGCCG
CGTGAGCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCCGGCGACCGCCGCTTCCG
GCCGCCACCAACCTGCGCAGCGTGTGCCCCTGGGCCTACAGAATCTCCTACGACCCGGCGA
GGTACCCCAAGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTC
GGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCGTGTCTACATGCCACCGTCGTCCTGCGCCG
CACCCCGCCTGCGCCGCGGGCCGCTTCCGTCTACACCGAGGCCTACGTCAACATCCCCGTGG
GCTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAA
CAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCC**TG**AGGCCGGTCTCTG
CCCCGGGAGGTCTCCCCGGCCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCTGGAGGGCTC
GGTCGGCGACCTCTGAAGAGAGTGCACCGAGCAAACCAAGTGCCGGAGCACCAGCGCCGCT
TTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCATCCCTGGCTTGCTTTTAGCTAC
AAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGGGCATCCTGTGTGCGGC
CCGCATGGAGGGTTTGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATCGGCTGCT
GCGGGTGCAGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTT
TTAAAGCAATCTAAAAATAATAAAGTATAGCGACTATATACCTACTTTTAAATCAACTG
TTTTGAATAGAGGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTA
ACATATAAACATCGTTTTTTACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTT
GGATAAATTTTGTAGCTGGTACACTCTGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGG
CTGACTGATGAAATGGACACGTCTCATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACG
GGCCTCCAGGTGGACCAAGGGATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGT
TCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGCACAATT
TTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGT
GGAACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGG
GCTTTAGGATCAGGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAAT
CTGGAGGCTTCTGTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATT
GAAAGTCTGTCTCTGAACACAATTATTTGTAAAAGTTAGTAGTCTTTTTTAAATCATTAAA
AGAGGCTTGCTGAAGGAT

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FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA173894
><subunit 1 of 1, 202 aa, 1 stop
><MW: 21879, pI: 9.30, NX(S/T): 2
MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQL
GPREQARNASCPAGGRPGDRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCL
TGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI
NSSIDKQGAKLLLGPNDAPAGP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 68-72;181-185

Tyrosine kinase phosphorylation site:

Amino acids 97-106

N-myristoylation sites:

Amino acids 17-23;49-55;74-80;118-124

Amidation site:

Amino acids 21-25

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FIGURE 89

CCGGGGCCTCCGGAGAACGCTGTCCCATGAACGTGCGGGGAGCGGGCCCCGGCGTCCGCGCG
TCCCCGCGTCCCTGGCAATTCCCAGACTTCCAACGGCTTCCCGCTGGCAGCCCCGAAGCCGC
ACC**ATG**TTCCGCTCTGGTTGCTGCTGGCCGGGCTCTGCGGCCTCCTGGCGTCAAGACCCGGT
TTTCAAAATTCAC TTCTACAGATCGTAATTCAGAGAAAAATCCAAACAAATACAAATGACAG
TTCAGAAATAGAAATATGAACAAATATCCTATATTATTTCCAATAGATGAGAACTGTACACTG
TGCACCTTAAACAAAGATATTTTTTAGCAGATAATTTTATGATCTATTTGTACAATCAAGGA
TCTATGAATACTTATTCTTCAGATATTCAGACTCAATGCTACTATCAAGGAAATATTGAAGG
ATATCCAGATTCCATGGTCACACTCAGCACGTGCTCTGGACTAAGAGGAATACTGCAATTTG
AAAATGTTTCTTATGGAATTGAGCCTCTGGAATCTGCAGTTGAATTTCAGCATGTTCTTTAC
AAATTAAAGAATGAAGACAATGATATTGCAATTTTTATGACAGAAGCCTGAAAGAACAACC
AATGGATGACAACATTTTTATAAGTGAAAAATCAGAACCAGCTGTTCCAGATTTATTTCTCT
TTTATCTAGAAATGCATATTGTGGTGGACAAAACCTTTGTATGATTACTGGGGCTCTGATAGC
ATGATAGTAACAAATAAAGTCATCGAAATTGTTGGCCTTGCAAATTCATGTTACCCCAATT
TAAAGTTACTATTGTGCTGTCATCATTGGAGTTATGGTCAGATGAAAATAAGATTTCTACAG
TTGGTGAGGCAGATGAATTATTGCAAAAATTTTTAGAAATGGAACAATCTTATCTTAACCTA
AGGCCTCATGATATTGCATATCTACTAATTTATATGGATTATCCTCGTTATTTGGGAGCAGT
GTTTCCTGGAACAATGTGTATTACTCGTTATTCTGCAGGAGTTGCATTGTACCCCAAGGAGA
TAACCTGGAGGCATTTGCAGTTATTGTCAACCCAGATGCTGGCACTCAGTCTGGGAATATCA
TATGACGACCCAAAGAAATGTCAATGTTCAGAATCCACCTGTATAATGAATCCGAAGTTGT
GCAATCCAATGGTGTGAAGACTTTTAGCAGTTGCAGTTTGAGGAGCTTTCAAATTTCAATTT
CAAATGTGGGTGTCAAATGTCTTCAGAATAAGCCACAAATGCAAAAAAATCTCCGAAACCA
GTCTGTGGCAATGGCAGATTGGAGGGAAATGAAATCTGTGATTGTGGTACTGAGGCTCAATG
TGGACCTGCAAGCTGTTGTGATTTTCAACTTGTGTACTGAAAGACGGAGCAAAATGTTATA
AAGGACTGTGCTGCAAAGACTGTCAAATTTTACAATCAGGCGTTGAATGTAGGCCGAAAGCA
CATCCTGAATGTGACATCGCTGAAAATTGTAATGGAAGCTCACCAGAATGTGGTCTTGACAT
AACTTTAATCAATGGACTTTCATGCAAAAATAATAAGTTTATTTGTTATGACGGAGACTGCC
ATGATCTCGATGCACGTTGTGAGAGTGATTTTGGAAAAGGTTCAAGAAATGCTCCATTTGCC
TGCTATGAAGAAATACAATCTCAATCAGACAGATTTGGGAAGTGTGGTAGGGATAGAAATAA
CAAATATGTGTTCTGTGGATGGAGGAATCTTATATGTGGAAGATTAGTTTGTACCTACCCTA
CTCGAAAGCCTTTCCATCAAGAAAATGGTGATGTGATTTATGCTTTCGTACGAGATTCTGTA
TGCATAACTGTAGACTACAAATTGCCTCGAACAGTTCAGATCCACTGGCTGTCAAAAATGG
CTCTCAGTGTGATATTGGGAGGGTTTGTGTAATCGTGAATGTGTAGAATCAAGGATAATTAAG
GCTTCAGCACATGTTTGTTCACAACAGTGTTCTGGACATGGAGTGTGTGATTCCAGAAACAA
GTGCCATTGTTCCGCCAGGCTATAAGCCTCCAAACTGCCAAATACGTTCCAAAGGATTTTCCA
TATTTCTGAGGAAGATATGGGTTCAATCATGGAAAGAGCATCTGGGAAGACTGAAAACACC
TGGCTTCTAGGTTTCTCATTGCTCTTCTCATTGTAACAACCGCAATAGTTTTGGC
AAGGAAACAGTTGAAAAAGTGGTTTCGCCAAGGAAGAGGAATTCCCAAGTAGCGAATCTAAAT
CGGAAGGTAGCACACAGACATATGCCAGCCAATCCAGCTCAGAAGGCAGCACTCAGACATAT
GCCAGCCAAACCAGATCAGAAAGCAGCAGTCAAGCTGATACTAGCAAATCCAAATCAGAAGA
TAGTGCTGAAGCATATACTAGCAGATCCAAATCACAGGACAGTACCCAAACACAAAGCAGTA
GTAAC**TAG**TGATTTCCTTCAGAAGGCAACGGATAACATCGAGAGTCTCGCTAAGAAATGAAA
TTCTGTCTTTCCTTCCGTGGTCACAGCTGAAAGAAACAATAAATTGAGTGTGGATC

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FIGURE 90

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA176775
><subunit 1 of 1, 787 aa, 1 stop
><MW: 87934, pI: 5.49, NX(S/T): 4
MFRLWLLLAGLCGLLASRPGFQNSLLQIVIEPEKIQTNTNDSSEIEYEQISYIIPIDEKLY
TVHLKQRYFLADNFMIIYLYNQGSMTYSSDIQTQCYQGNIEGYPDSMVTLSLSTCSGLRGI
LQFENVSYGIEPLESAVEFQHVLYKLKNEEDNDIAIFIDRSLKEQPMDDNIFISEKSEPAV
PDLFPLYLEMHIVVDKTLTYDYWGSDSMIVTNKVIEIVGLANSMTQFKVTIVLSSLELWS
DENKISTVGEADELLQKFLEWKQSYLNLRPHDIAYLIIYMDYPRYLGAVFPGTMCITRYS
AGVALYPKEITLEAFVIVTQMLALSLGISYDDPKKCQCSESTCIMNPEVVQSNQVKTFS
SCSLRSFQNFISNVGVKCLQNKPMQKKSPPKFCVGNRLEGNEICDCGTEAQCGPASCCD
FRTCVLKDGAQCYKGLCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGBPITLING
LSCKNNKFICYDGDCHDLARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGDRNNKYV
FCGWRNLICGRVLCTYPTKPFHQENGDVIIYAFVRDVSVCITVDYKLPRTVPDPLAVKNGS
QCDIGRVCVNRECVESRIKASAHVCSQQCSGHGVCDNRNKHCHSPGYKPPNCQIRSKGF
SIFPEEDMGSIMERASGKTENTWLLGLIALPILIVTTAIVLARKQLKKWFAKEEEFPSS
ESKSEGSTQTYASQSSSEGSTQTYASQTRSESSSQADTSKSKSEDSAEAYTSRSKSDST
QTQSSSN
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 309-326;681-705

N-glycosylation sites:

Amino acids 39-43;125-129;465-469;598-602

Glycosaminoglycan attachment site:

Amino acids 631-635

Tyrosine kinase phosphorylation site:

Amino acids 269-276

N-myristoylation sites:Amino acids 13-19;82-88;99-105;218-224;401-407;634-640;
726-732;739-745**EGF-like domain proteins:**

Amino acids 642-654

Disintegrins proteins:

Amino acids 400-407;422-472;403-453;467-517;634-684

Reprolysin (M12B) family zinc metalloprotease:

Amino acids 186-383

Reprolysin family propeptide:

Amino acids 63-176

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FIGURE 91

CACCAGACAGCACTCCAGCACTCTGTTTGGGGGGGCATTGCGAAACAGCAAAATCACTCATAAA
AGGCCAAAAAATTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGAAAAG
ACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTGAGCTTGTTCACCTCAG
CTGGGAATGTCATCAGGCAACTCAAGTTTTTACCACGGCATGTGTCTGTGAATGTCCGCA
AAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGG
ATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTT
CTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAACAGTT
ATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACAACC
AATAGTTCTACAAGTGAAAATCGTGCTTCGTGCTCTTTTTTCTTCCAAGAATAACGATCCC
AGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAAATTAAATCTCATATGA
CATACTGGAGATTAGAGAACATAGCGAAAACCTGAACCACCTAAGATTTTCCGTGTGAAACCA
GTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCTGAGTTGGCGCCTGTTTC
ATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGCTGGATGGAAGTCA
ACTTCGCTAAGAACCGTAAGGATAAAAACCAAACGTACAACCTCACGGGGCTGCAGCCTTTT
ACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGTCAAAGTTCTGGAGTGAAGTGGAG
CCAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCCATGTGGCCTGGAAGTGTGGAGAGTCC
TGAAACCAGCTGAGGCGGATGGAAGAAGGCCAGTGCAGTTGTTATGGAAGAAGGCAAGAGGA
CCCCCAGTCCTAGAGAAAACACTTGGCTACAACATATGGTACTATCCAGAAAGCAACACTAA
CCTCACAGAAACAATGAACACTACTAACAGCAGCTTGAAGTGCATCTGGGAGGCGAGAGCT
TTTGGGTGTCTATGATTTCTTATAATTCTCTTGGGAAGTCTCCAGTGGCCACCTGAGGATT
CCAGCTATTCAAGAAAAATCATTTCAGTGCATTGAGGTGATGCAGGCCTGCGTTGCTGAGGA
CCAGCTAGTGGTGAAGTGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGT
TTCCGGATGTGGACTCAGAGCCCACCACCTTTTCTGGGAATCTGTGTCTCAGGCCACGAAC
TGGACGATCCAGCAAGATAAAATTAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAAT
GTTGCATGACAAAGTTGGCGAGCCATATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCAT
CAGAAGGTCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAA
GAGATTCCCAAGAGTGAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGA
AGGTGGAAAAGGATTCTGTAAGCACGCCCATAGCGAAGTGGAAAAAACCACAGCCCCAGA
TAGATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCCATCTCATTGTGACTTGCAACCT
GGCATGAATCACTTAGCTTCTTTAAATCTCTCTGAAAATGGGGCCAAGAGCACCCACCTTTT
GGGGTTTTGGGGTTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGAGTCTGAGGAAAT
GGAAGGAGTTGTTATAATTTGTCCTGGTTAGGCCCTGAATTGACCTCCCGGGAGCTCCCCGA
CCATCATTTCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCCTGTCACCA
TGACTTCTACTGCCCTGCCAAATCATGCTTTTGTGTTTTTCAGTCCACCTTATCTCCTGACATCT
TAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTTCTTATGGTAAAATA
CACGTAAAATATTTTTCCAGTTTAAACATTTGAAAGTGTACAATTTAGTGGCATTAGAAGCA
TTCACAATATTGTGCAACCATCACCCTATTTCCAGAACTCTTCTATTTCTGCCCAAATAGA
AGCCCTATACCCATTCATTAGTCACTCCCATTCCTCTCCTCCACAGCCCTGGCAACTAC
CAAAGTCTTTGTGTCTCTATGGATTGCCTATTTTGGATATTTTATATACATAGAATCATAA
ANTAAAAA

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FIGURE 92

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA177313
><subunit 1 of 1, 582 aa, 1 stop
><MW: 66605, pI: 8.14, NX(S/T): 15
MCIRQLKFFTTACVCECPQNILSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENI
SCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTNSSTSENRASCSFFLPRI
TIPDNYTIEVEAENG DGVIKSHMTYWRL ENIAKTEPPKIFRVKPVLG IKRMIQIEWIKPE
LAPVSSDLKYTLRFRTVNSTSWMEVNF AKNRKDKNQTYNLTGLQPFTEYVIALRC AVKES
KFWS DWSQEKMGMT EEEAPCGLELWRVLKPAEADGRRPVRL L WKKARGAPVLEKTLGYNI
WYYPESNTNLTETMNTTNQQLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQC
IEVMQACVAEDQLVVKWQSSALDVNTWMI EWFPD VDSEPTT LSWESVSQATNWT IQQDKL
KPFWCYNISVYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKT V TITWKEIPKSE
RKGIIICNYTIFYQAEGGKGFKHAHSEVEKNPKPQIDAMDRPVVGMAPP SHCDLQPGMNH
LASLNLS ENGA KSTHLLGFWGLNESEVTV PERRVLRKWKELL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 59-63;69-73;99-103;103-107;125-129;198-202;
215-219;219-223;309-313;315-319;412-416;
427-431;487-491;545-549;563-567

N-myristoylation sites:

Amino acids 32-38;137-143;483-489;550-556;561-567

Amidation site:

Amino acids 274-278

Growth factor and cytokines receptors family signature 1:

Amino acids 62-75

Fibronectin type III domain:

Amino acids 54-144;154-247

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FIGURE 93

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTTACCATCT

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FIGURE 94

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57700
<subunit 1 of 1, 125 aa, 1 stop
<MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAI
LSLKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRCTRNR
HVLYP
```

Important features:**Signal peptide:**

Amino acids 1-21

N-myristoylation sites:

Amino acids 33-39;70-76

Anaphylatoxin domain proteins:

Amino acids 50-60

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FIGURE 95

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTCATGCTTCCTGTGATTC
ATCCAAC TACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 96

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62872
<subunit 1 of 1, 90 aa, 1 stop
<MW: 9039, pI: 4.37, NX(S/T): 1
MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPT
ATTAASTTARKDIPVLPKWVGDL PNGRVCP

Important features:**Signal peptide:**

Amino acids 1-19

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FIGURE 97

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAA**AACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 98

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62876
<subunit 1 of 1, 120 aa, 1 stop
<MW: 12925, pI: 9.46, NX(S/T): 0
MLPPALPPALVFTVAWSLLAERVSQVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGR
AGGGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

Important features:**Signal peptide:**

Amino acids 1-17

N-myristoylation sites:

Amino acids 58-64;63-69;64-70;83-89;111-117;115-121

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FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66660
><subunit 1 of 1, 209 aa, 1 stop
><MW: 21588, pI: 5.50, NX(S/T): 0
MRSTILLFCLLGSTRSLPQLKPAALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQML
TLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEELP
QIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLEPAGGAGVNPATQGTTPAGRLPTPSGTDD
DFAVTTPAGIQRSTHAIEEATTESANGIQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Leucine zipper patterns:

Amino acids 10-32;17-39

N-myristoylation sites:Amino acids 12-18;25-31;36-42;74-80;108-114;111-117;
135-141;151-157;159-165;166-172;189-195

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FIGURE 101

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCTTTATACAATG

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FIGURE 102

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQV
EWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIP
FLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTA
SLQPGISEDLLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRKFARMIEQRAVDTSLYILPKEDRES
LQMAVGPFLLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDCHKWPPFAVDLTMELYQHLESK
EWFVQLYYHGKEQVPRGCPDGLCPDMLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 103

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCGCGCTCCCTGCGCCGCGCGCCGCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCGCCAGGGGACCACGGTGGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCAATTGCCAGCTGCGGCCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCACCA
CGAGGCCCGTGGTGCGGGAGCCCACAGCCTTGTCTTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTACGCCCAGGCCACCACTCCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGACGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAACGGAGGGAGTGAAGGTC
CCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
ATAAAAAAAAAA

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FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

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FIGURE 105

CCCACGCGTCCGAAGGCAGACAAAGGTTTCATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

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FIGURE 106

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHF
DGKGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:**Signal peptide:**

Amino acids 1-20

N-glycosylation site:

Amino acids 72-76

Tyrosine kinase phosphorylation site:

Amino acids 63-71

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FIGURE 107

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGTA
TCCCCCGAGAGCAGAATAGGTACTCCACTCCGGACTCCTGGACTGCATTAGGAAGACCTCT
TTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTA
ACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCAT
AGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTC
CTACATTAAAAATATAATGTCTCTCTCTATTCCCTCAACAATAAAGGATTTTGCATATGAAA
AA

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FIGURE 108

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59849
<subunit 1 of 1, 135 aa, 1 stop
<MW: 14833, pI: 9.78, NX(S/T): 0
MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGL
LKALSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLG
STGKSSLGTEEQRPL

Important features:**Signal peptide:**

Amino acids 1-18

Tyrosine kinase phosphorylation site:

Amino acids 36-45

N-myristoylation sites:

Amino acids 33-39;59-65

Amidation site:

Amino acids 90-94

Leucine zipper pattern:

Amino acids 43-65

Tachykinin family signature:

Amino acids 86-92

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGACGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCC**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAFKEKYMFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

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FIGURE 111

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGTTTCTTAATTTCCACA

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FIGURE 112

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPR
FPWFRRNFPIPIPIESAPTTPLPSEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Homologous region to B3-hordein:

Amino acids 47-85

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FIGURE 113

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAAA

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FIGURE 114

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSVPVEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340**N-myristoylation site.**amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292**Amidation site.**

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 115

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTATAA
GAGATGATGGAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

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FIGURE 116

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896
<subunit 1 of 1, 166 aa, 1 stop
<MW: 19171, pI: 8.26, NX(S/T): 1
MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQSKK
PLMVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIM
FVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL
```

Important features:**Signal peptide:**

Amino acids 1-23

N-myristoylation site:

Amino acids 51-57

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FIGURE 117

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCGCGATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTACAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCAAT**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGGAAC
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT
CCACTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTGTTGATCCTGGTTCTTTTCGGCCGT
TCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGG
CGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGC
AGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGT
GTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGATGCCTCAGTTCTTGGAAGCTA
GGTTCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCC
CCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAG
GGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACT
CATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGAC
GTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTGG
TGTTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAGG
GACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATCC
CCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTTT
GTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGCC
CATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTAG
TTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

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FIGURE 118

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920
><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSSARAEGAEPPAPEPSAGASSNWTTL
PPPLFSKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK
ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGT
TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPILIGQKLSEMD
SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP
GDIRHPKHVQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 58-76

N-glycosylation sites:

Amino acids 56-60;194-198

N-myristoylation sites:Amino acids 6-12;52-58;100-106;125-131;233-239;270-276;
275-281;278-284**Amidation site:**

Amino acids 154-158

Cell attachment sequence:

Amino acids 205-208

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FIGURE 119

GCCCACGCGTCCGATGGCGTTTCACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGG
TGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTT
GGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACC
AAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTT
ACTTTAAAAAATGACTCCTTATTTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTGT
TTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATG
ATTACCTCTGGTGTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTGA
ATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATATAGGAACCTTGTAG
GGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCT
TCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTCA
TGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTTG
AATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAAT
ATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTTG
TGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTGTGAAGACATTACTTATTAAGA
AATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGT
ACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGTG
CAATACAATAAACTCTGAAATTAAGACTC

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FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA
FFCVMFLCAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW
CKLAFYLLAFFYYLYGMIYVLVSS

Important features:**Signal peptide:**

Amino acids 1-20

Type II transmembrane domain:

Amino acids 11-31

Other transmembrane domain:

Amino acids 57-77;123-143

Glycosaminoglycan attachment site:

Amino acids 96-100

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FIGURE 121

CGGACGCGTG GGGCGGACGCGTG GGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCGTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACCCACATCCCCACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 122

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHHLKCV DIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCS PGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVLV LQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 123

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCC
TCTACATGCGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCAC
AACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCA
CCCCCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCA
TGTACACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTTCGATCCGTGAGGAGAGCAGC
TACAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTA
CTCCAAGCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGT
GGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTC
AGTGGCATCCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCCCTCAAGCTGGAGCTGATCCCCGACGTGAC
CATCCCCGCCAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAG
CGCCTGCGCTGGCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCG
CTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGAGAACAACCGCTA
CATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGC
CACAGGTGGTACAGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTC
CTCAACAGCCTCAAGAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCA
CTCCATCTTCAGCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCA
TCAGCTTCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAG
ATCGGCAACCTCACCAACCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTT
CTACTGCCGCAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCC
TGAGAACCTCCAGAACCTAGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGG
AAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCT
GACGCAGATCGAGCTGCGGGGCAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGGCCACTGCTCAAGC
GCAGCGGCTTGGTGGTGGAGGAGGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCT
GACAAGGAGCAGGCTGAGCGGAGGCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGG
AGGGGCGAGGCTAGCTTCTCCAGAACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCC
GCTTGTGAGTCAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCAGCTC
GCTTCCAGCAAGTCTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTG
GAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCTTGGACCCCTCACTTTAGTTCTTGGTATTTAT
TTTTCTCCATCTCCACCTCCTTCATCCAGATAACTTATACATTCCCAAGAAAGTTAGGCCAGATGGAAGGTG
TTCAGGGAAAGGTGGGCTGCCTTTTCCCTTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGG
ACTTCAGCAGAGTGGTCCGGGGCGAACAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTG
CGGTCCACGGGAGAGCAGGCTCCAGCTGGAAGGCCAGGCTGGAGCTTGCTCTTCAGTTTTGTGGCAGTT
TTAGTTTTTTTGTTTTTTTTTTTTTTAAATCAAAAAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTT
GGGTATTAATAAGAAAAAAACTTAAAAAAAGACACTAACGGCCAGTGAGTTGAGTCTCAGGGCAGG
GTGGCAGTTTCCCTTGAGCAAAGCAGCCAGAGCTTGAAGTGTGTTTCTTTCCCTGGGCGCAGGGTGCAGGGTG
TCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTTCTATTTGTTCTTGGGAGGGAGGTTTTTTTGTGTTTT
TTGGGTTTTTTTGGTGTCTTGTGTTTTCTTCTCCATGTGCTTGGCAGGCACTCATTCTGTGGCTGTGGC
CAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTCGGGTTGGCTAATCCCCGATGAACGGTGTCTCA
TTCGCACCTCCCTCCTCGTGCCTGCCCTGCCTCTCCACGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGC
CCAGACTTTGTTTTCCCACTCCTGCGGCATGGGTGTGTCCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAG
CCCTGTGCCACCTGGTCTTCATGAAGAGCAGACACTTAGAGGCTGGTGGGAATGGGAGGTGCCCCCTGGG
AGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGCTGGAGTGCACACAGCCAGTGGGCACCTGGTG
GCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCCGCTTAGATCAATCAGTGG
ACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGTCCATCCGTCTGTCCGTCCATTTGTGTTTTCT
GCGTCGTGTATTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAAATCCGTT
ACATGTGGGTCTGAACTGTAGACTCGGTACAGTATCAATAAAATCTATAACAGAAAAA

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FIGURE 124

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTEELHLTGNLSEAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 125

GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAATATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAAATCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAACACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 126

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNR
VTRVAWLN RSTILYAGNDKWCLDPRV VLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVR RVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKGV KVENRPF LSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Important features:**Signal peptide:**

amino acids 1-28

FIGURE 127

GGGCGCGGTGCACCGGGCGGGCTGAGCGCCTCTGCGGCCCGGCTGCGCGCCCCGGCCCGCGCGCCAGGTGAGCGCTCCG
GCCCCAACCCCGGCGCGCCCTAGCCCCCGCGGGCCCGCGCCCGCGCCAGGTGAGCGCTCCG
CCCGCGCGAGGCCCCCGCCCGCGCCCGCCCCCGCCCGCGCGCGCGGGGGAACCGGGCGGATTCTCTCGCG
CGTCAAACCATCTGATCCCATAAAATTTCATCTCCCGCGCGCCGCTGCGAGCGCCCCGAGTCCGCGC
CGCGCGCGCCTCGCCTGTGCGCCTGCGCGCCTGCGCACCCGCGCGCCGAGCCAGCCAGAGCGCGGCGGA
GCGGAGCGCGCGAGCCTCTGTCGCGCGCGGGCGGGGCGGGGCGGTAGCGCGCGCGCTGGATGCGGACCCG
GCCGCGGGGAGACGGGCGCCCGCCCCGAAACGACTTTCAATCCCCGACGCGCCCCGCCCAACCCCTACGATGAA
GAGGGCTCTCCGCTGGAGGAGCGGGCTGTGGCATGGGTGCTGTGGCTGACGGCCTGGCAGGTGGACGCCCAT
GCCAGGTGCTTGGATATGCTACAATTGACCCAAAGTGACGACAAGTGTGCCCCAGAGGGCCTGACGGCTGTG
CCCGTGGGCATCCCTGCTGCCAGCCAGCGCATCTTCTGTCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAG
CTTCCGTGCTGCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCGAATTGATGCGGCTGCCT
TCACTGGCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCAACAGCTCCGGTCTGTGGACCCCTGCCACA
TTCACGGCCTGGGCGCCTACACAGCTGCACCTGAGACCGCTGCGGCTGACGGAGCTGGGCGCGGGCTGTT
CCGCGCCTGGCTGCCCTGCAGTACTCTACTGCAAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCC
GCGACCTGGGCAACCTCACACACCTCTTCTGCACGGCAACCGCATCTCCAGCGTGGCCGAGCGCGCCTTCCGT
GGGCTGCACAGCCTCGACCGTCTCCTACTGCACCGAACCAGCTGGCCCATGTGCACCCCGACCTTCCGTGA
CCTTGGCGCCTCATGACACTCTATCTGTTTGCACCAATCTATCAGCGCTGCCCATGAGGCCCTGGCCCCC
TGGTGCCCTGCACTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGACAGCCCATCTGGGCG
TGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCT
CAAACGCCTAGCTGCCAATGACTGCAGGGCTGCGCTGTGGCCACGGGCCCTTACCATCCATCTGGACCGGCA
GGGCGACCGTAGGAGAGCGCTGGGGCTTCCCAAGTGTGCCAGCCAGATGCCGTGACAAGGCCCTCAGTACTG
GAGCCTGGAAGACAGCTTCCGAGGCAATGCGCTGAAGGACGCGTGCCGCGGCTGACAGCCCGCGGGCAA
CGGCTCTGGCCCAGGCGCATCAATGACTACCCCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCGCTCACTG
CAGTGCGGCGCGAGGGCTCCGAGCCACAGGGTTCCTCCCTCGGGCCTCGCCGAGGCCAGGCTGTTACGC
AAGAACCGCACCCGACGCCATCGGCTCTGGGCGAGGACGAGCGGGGTGGCGGACTGGTGACTCAGAAGG
CTCAGTGCCCTACCCAGCCTCAGCTGCAGCTCACCCTCGGCTGGGCTGGCGTGGTGTGTGACAGTGCTTG
GCGCCTGCTGACCCCCAGCGGACACAGAGCGTGTCTCAGCAGCCAGGTGTGTGTACATACGGGCTCTCTCCA
CGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCTGATGGACGCTGCGGCC
CGCCACCCCATCTCCACCCCATCATGTTTACAGGTTTGGCGGCGAGCGTTTGTTCAGAACGCCGCTCCAC
CCAGATCGCGGTATATAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGAGCTGGAATAAAGAGC
CTTTTTCTAAAAA

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FIGURE 128

MKRASAGGSRLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIFLHG NRISHVPA
ASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPATFHGLGRLHTLHLDR CGLQELGPG
LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHG NRISVPERAFRGLHSLDRLLLHQNRVAHVH PHAF
RDLGRLMTLYLFANNLSALPTEALAPLRALQYLR LNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGR
DLKRLAANDLQGC AVATGPYHPIWTGRATDEEPLGLPKCCQPD AADKASVLEPGRPASAGNALKGRVPPGDSPP
GNGSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGTGDS
EGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 129

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCCGGCTCCCGCCCGGCACATGGCTGCAGCCAC
CTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCGAGGTCCGTCCGAGGCGCCCGGCCGCCCGGAGCCAA
GCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATCGGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCC
TACTATGTTGGAACCTTGGGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGGCCTGCCA
CCATCAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAAACAAA
AAGTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGAAGGAGAACAGAAAGGGCCGAGTGGCCTTT
GCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGCCAGTGATGAGGGCCGGTACAC
CTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCTATCTTAAAGTCTTAGTGAGACCATCCAAGC
CCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACA
GAGCCCATTTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAG
GATTGACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTACCAGTGCA
CAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTCCGAGTAAGTGTACAGTATGTACAAAGCATCGGCATG
GTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTGTGGCTGCTAATCCGAAG
GAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCC
GTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTCTTCTCCTCCACTCGCTCCACA
GCAATAGTGCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGC
ATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGCAG
AAACCACACCCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAAACGGTCTGAATTACAATGGACTTGACTCCC
ACGCTTTCTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGAT
GAGAGGTCATCTAAGTAGCAGTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATACAAATACCAA
CAAGCAAAAGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAG
CAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAATATACCTAA
AACTTTTAATGTGGGATATTTGTATCAGTGCTTTGATTGACAATTTTCAAGAGGAAATGGGATGCTGTTTGTA
AATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTAT
TACACCTGTCTACACCATGTACTGAGCTAACCATTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATT
CTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAG
AGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAACTATGAAAGGAGACA
AAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAA
ATATATAATGGAGCAATTGTGGATTCCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGG
AAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAAT
GCTGAAAGATTACCAACATACCATATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAAATGCAAGACTGG
GTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCA
CCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAG
AGCGGGACTCCGTCTC

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FIGURE 130

MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVITYSSRHVYNN
LTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELTEGSD
LTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVR
VTVQYVQSIGMVAGAVTGIVAGALLIFLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRS
SRSGSSSTRSTANSASRSQRTLSTDAAPQGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important features:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 131

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC
AGTCCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTCTCTTTTGGGCTTATCTCTGGCG
GGCGCGGCGGAACCTAGAAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG
TTCCAGAGGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATTGAACATAAAAAACAACCTCGATTTTCGAAAACTTCAGTCTCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTTAGTGTTTCAGATCTTGATTACAGGAG
AAAATGGGAAAATTAGTTGCTCCATTACAGGAGGATCTACCCCTCCTCCTGAAATCCGCGGAA
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTACCCCAAACCTCCTACACCCTGTTTCGTC
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
CACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGGTTCCAGTTCGCGGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGCGGTGGTGGTCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGGAGCCGGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCGTACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTGGCGGTGTGGGCGCACAAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCCAGGCCGACTTGCTCACCG
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTGGTGCCGA
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCCAGAGCTACC
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATT
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
TTACTCTGATTTTTCTCATGTTCTTTCTCCCTTGTGTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

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FIGURE 132

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVS RGNKHLQLNQETADLLLNEKLDREDLCGHTEPCVLR FQVLLES PF EFFQ AELQV
IDINDHSPVF LDKQMLVKVSESSPPGTT FPLKNAEDLDVGQNNIENYII SPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVD TG VNGEISYS L FQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDH APEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLLKSAENFYTL LTERPLDRESRAEYNITITVTDLGT PMLITQ
LNMTVLIADVNDNAPAF TQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVL DANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELG LFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPFPQCPGKEIQGNSTFPNNFGENIQ
```

Important features:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

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FIGURE 133

GGAAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTG
ACACAGGCTGGAGTGCAGTGGTGTGATCTTGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATG
CCTCAGCCTCCCGAGTAGCTGGGATTACAGTGGTGAAGTACTCCAGAGTGAAGTCCGTCGGAGGAAAATGACTCCC
CAGTCGCTGCTGCAGACGACACTGTTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCA
CAGGGAAGACTTTTCGCTTCTGCAGCCAGCGGAACAGACACAGGAGCAGCCTCCACTACAAACCCACACCAG
ACCTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTTCCCTGCAGCCACCCCTGCT
TCCCAGTCCCTTCCCTGACCCAGGGGCCCTTACCCTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACA
TCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGG
AGAGCCTGGCTCAGGGCCCCCGCTGTTAGCCACTTCTGTCACTCCTGGTGGAGCCCTCAGAACATCAGCCTG
CCCAGTGCCGCCAGCTTACCTTCTCCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACAT
GTGCGAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCCTCAAGGAGGCCCT
CGGCTGCCCCGCCAGCCAGCAGTTCAGAGCCTGGAGTCAAACTGACCTCTGTGAGATTATGGGGGACATG
GTGTCCTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAAGCTCCAGCCACAGCCCGCCTCCAGGACCTGCA
CATCCACTCCCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCC
AGAGGACGAAAGGCCGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTC
CAGGACAAGAATTCAGCCAAGTCCCTGGGTGAGAAGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAA
CCTCAGGAGCCCGTGGTGTCTACTTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCT
GGGTTGAAGACCCACATTGAGCAGCCCGGGGCAATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACC
CAAACATCCTGCTTCTGCAACCACTTGACCTACTTTGAGTGTGATGGTCTCCTCGGTGGAGGTGGACGCCGT
GCACAAGCACTACCTGAGCCTCCTCTCCTACGTGGGCTGTGTCTCTGCCCTGGCCTGCCTTGTCAACATTG
CCGCCTACCTCTGCTCCAGGGTGCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGTGCACATG
AACCTGCTGCTGGCCGTCTTCTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGA
GGCTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTCACCTGCCTTTCTGGATGGGCCCTGAGG
GGTACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCC
ATGGGCTGGGGCTTCCCCTCTTTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCAT
CTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCACT
ACATCACCACCTGGGCCCTCTCAGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAG
ATCCTGCGGCTGCGCCCCACACCCAAAGTGGTGCATGTGCTGACACTGCTGGGCTCAGCCTGGTCTTGG
CCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTCTGGCACCTTCCAGCTTGTCTCTCTACCTTTTCAGCA
TCATCACCTCCTTCCAAGGCTTCTCTCATCTTCTGTTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCC
TCCCCTCTGAAGAGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACTCGTCCAGCCGCATCTA
GGCCTCCAGCCACCTGCCATGTGATGAAGCAGAGATGCGGCCTCGTCGACACTGCCTGTGGCCCCGAGCC
AGGCCAGCCCCAGGCCAGTCAAGCCGAGACTTTGGAAGCCCAACGACCATGGAGAGATGGGCCGTTGCCATG
GTGGACGGAATCCCGGGCTGGGCTTTTGAATTGGCCTTGGGGACTACTCGGCTCTCACTCAGTCCACGGGAC
TCAGAAGTGCGCGCCATGCTGCCTAGGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGGCCCTGGTCTCT
CCTTACAACCCCTGGGCCAGCCCTCATTGCTGGGGCCAGGCCCTGGATCTTGAGGGTCTGGCACATCCTTAA
TCCTGTGCCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCAACCTGAGGGCACTCTG
CATCTCTGTCAATTTAACTCAGGTGGCAGCCAGGGCGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCC
CTGGCGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGCAGCTCGCCTACCTCTGAGCCAGGCCCTCCCTCC
CTCAGCCCCCAGTCTCTCCCTCCATCTTCCCTGGGGTCTCCTCCTCTCCAGGGCCTCCTTGTCTCCTTCTGTT
ACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAA
ATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGGGCTAGGTC
CCTCTGTCCATCTGGGCTTTGTATGAGCTGCATTGCCCTTGCTCACCTGACCAAGCACACGCCTCAGAGGGG
CCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGGACCATGCCAGTCCGCTCTGGTTTCCATCCCAC
CACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTC
CAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCATCATGGTTAATTCTGTCCAACAAACACACGGGTA
GATTGTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTCACTCTG
GTATGTGAGGCGTGCCTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCATCATTCCTGCCTGGGAATC
CTGGAAGACTTCTGCAAGGAGTCAAGCTTCACTTGAACCTTGAAGATGGGAAGGATGTTCTTTTACGTACCA
ATTCTTTTGTCTTTTGTATTTAAAAAGAAATCATGTTTCACTGTAGAGAATTTGGAAGCTGTGAAGAGAAATCA
AGAAGAAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 134

MT PQSLLQTTLFLLSLLFLVQGAHGRGHREDFR FCSQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRD FLLSOKASSLLCFQH
QEESLAQGPPLLATSVTSWWS PQNISLPSAASF TFSFHSPPH TAAHNASVDMCELKRD LQLL
SQFLKHPQKASRRPSAAPASQQ LQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLAVFLDTS FLLSEPVALTGSEAGCRASAI FLHFSLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITS FQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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FIGURE 135

GCCTAGCCAGGCCAAGAATGCAATTGCCCGGTGGTGGGAGCTGGGAGACCCCTGTGCTTGGACGGGACAGGGTCGG
GGGACACGCAGGATGAGCCCCGCGACCACTGGGCACATTCTTGCTGACAGTGTACAGTATTTTCTCCAAGGTACA
CTCCGATCGGAATGTATACCCATCAGCAGGTGTCCTCTTTGTTTCATGTTTTGGAAAGAGAATATTTTAAGGGGG
AATTTCCACCTTACCCAAAACCTGGCGAGATTAGTAATGATCCCATAACATTTAATACAAATTTAATGGGTTAC
CCAGACCGACCTGGATGGCTTCGATATATCCAAAGGACACCATATAGTGATGGAGTCCTATATGGGTCCCCAAC
AGCTGAAAATGTGGGGAAGCCAACAATCATTGAGATAACTGCCTACAACAGGCGCACCTTTGAGACTGCAAGGC
ATAATTTGATAATTAATATAATGTCTGCAGAAGACTTCCCGTTGCCATATCAAGCAGAATTCCTCATTAGAAT
ATGAATGTAGAAGAAATGTTGGCCAGTGAGGTTCTTGAGACTTTCTTGCGCAGTGAAAAATGTGTGGCAGCC
AGAGCGCCTGAACGCCATAAACATCACATCGGCCCTAGACAGGGGTGGCAGGGTGCCACTTCCCATTAATGACC
TGAAGGAGGGCGTTTATGTCATGGTTGGTGCAGATGTCCCGTTTTCTTCTTGTTTACGAGAAGTTGAAAATCCA
CAGAATCAATTGAGATGTAGTCAAGAAATGGAGCCTGTAATAACATGTGATAAAAAATTTCTGACTCAATTTTA
CATTGACTGGTGCAAAATTTTCATTGGTTGATAAAACAAAGCAAGTGTCCACCTATCAGGAAGTGATTCGTGGAG
AGGGGATTTTACCTGATGGTGGAGAATACAAACCCCTTCTGATTCTTTGAAAAGCAGAGACTATTACACGGAT
TTCCTAATTACACTGGCTGTGCCCTCGGCAGTGGCACTGGTCCTTTTTCTAATACTTGCTTATATCATGTGCTG
CCGACGGGAAGGCGTGGAAGAGAAACATGCAACACCAGACATCCAACCTGGTCCATCACAGTGCTATTCAGA
AATCTACCAAGGAGCTTCGAGACATGTCCAAGAATAGAGAGATAGCATGGCCCTGTCAACGCTTCCTGTGTTT
CACCTGTGACTGGGGAAATCATACCTCCTTTACACACAGACAACATATGATAGCACAAACATGCCATTGATGCA
AACGCAGCAGAACTTGCCACATCAGACTCAGATTCCCCAACAGCAGACTACAGGTAAATGGTATCCCTGAAGAA
AGAAAAGTACTGAAGCAATGAATTTATAATCAGACAATATAGCAGTTACATCACATTTCTTTTCTCTCCAAT
AATGCATGAGCTTTTCTGGCATATGTTATGCATGTTGGCAGTATTAAGTGTATACCAATAATACAACATAACT
TTCATTTTACTAATGTATTTTTTTGTACTTAAAGCATTTTGTACAATTTGTAAACATTGATGACTTTATATTT
GTTACAATAAAAGTTGATCTTTAAATAAATATTATTAATGAAGCCTAAAAAAAAAAAA

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FIGURE 136

MQLPRWWELGDPCAWTGQGRGTRRMSPATGTGFTLLTVYSIFSKVHSDRNVYPSAGVLFVHVLEREYFKGEFPPY
PKPGEISNDPITFNTNLMGYPDPRGWLRYIQRTPYSDGVLYGSPTAENVGKPTIIETAYNRRTFETARHNLII
NIMSAEDFPLPYQAEFFIKNMNVEEMLASEVLGDFLGAVKNVWQPERLNAINITSALDRGGRVPLPINDLKEGV
YVMVGADVPFSSCLREVENPONQLRCSQEMEPVITCDKKFRTQFYIDWCKISLVDKTKQVSTYQEVIRGEGILP
DGGEYKPPSDSLKSRDYYTDFLITLAVPSAVALVFLILAYIMCCRREGVEKRNMQTPDIQLVHHSIAIQKSTKE
LRDMSKNREIAWPLSTLPVFHPVTGEIIPPLHTDNYDSTNMPLMQTQQNLPHQTQIPQQOTTGKWYP

signal sequence:

Amino acids 1-46

transmembrane domain:

Amino acids 319-338

N-glycosylation site:

Amino acids 200-204

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 23-27

Tyrosine kinase phosphorylation site:

Amino acids 43-52

N-myristoylation sites:

Amino acids 17-23;112-118;116-122;

185-191

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FIGURE 137

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCA**ATGG**CTCCGCAGAACCTGAGCACCTTTT
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAATAAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
TGGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
TCACTTTTGTATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGAG**AGTG
AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGAAAAGAATGACC
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAAGAAACACAATATAGAGGGTTGGA
GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
TTATTTTTTA

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FIGURE 138

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFDLGAAY
EVLSNSEKRRKQYDTYGEGLKDGHQSSHGDISSHFFGDFGFMFGGTFRQQDRNIPRGSDIIVDLEVTLEEVYAG
NFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCECPNVKLVNEERTLEVEIEPGVRDGMET
PFIGEGERPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPG
AKLWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 139

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACC**ATG**CGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCTGTCCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTG**TAG**AGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 140

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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FIGURE 141

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
GCCCCCTCGGGAATCACAAC TGGGTACAAGACATTTTCGCCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTC
AGCT**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTGCTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCTGCCTTCCTGCTCACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCCC
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLEFVACLSLGGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVFPRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 143

GTGGGATTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGGCAGATGTTGGGG
CTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAA
AAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACC
ATAACTTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATA
GACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATC
TGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACACTCGCTCCAATGTGATTTTCT
ACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGGAATCCAT
GAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATG
ATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTT
TCAGAAGATTGTGATTTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTA
TCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTT
TTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGTA
GAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACA
GCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGT
TTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGAT
GTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAA
CATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACA
AACTGCCCTGTCTGCCAGTCAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGT
GTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAT
TCAAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTTC

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FIGURE 144

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 145

AAACTTGACGCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACCTCAATAAAACATTTTCCATCCAAA

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FIGURE 146

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLGKGLRSATPDAQ

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FIGURE 147

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

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FIGURE 148

MKFTIVEAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNGFAATRLFQKKTCTIVHKMNKEVMPSIQSLDALVKEKKLQGKPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 149

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGTTTGGG
GTTTATGCAAAATGAGTGTGTTTGTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 150

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAQPPPPITYSL
CGTKNIKVAKKVVKTHERPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPIALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 151

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 152

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

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FIGURE 153

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCCTGATCACTT
ATATCTGGAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAAAAA

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FIGURE 154

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPSLKCQ
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHRLVLKGPDLHLYLETKTLQGTKGENSLSSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP
ATCGGGYQLTSAECYDLRSNRVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKL PVEAKLPWFKQAQEELEGA AVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 155

[illegible]

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FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNRYRGQSSWGS CGGDAVGGVNTVNSE TSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 157

[illegible]

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FIGURE 158

MDFLLLGICLYWLLRRPSGVVLCILGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHNLSGLLGLSLRY
NSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQITQLPNTTFRMPENLRSVDLSYNK
LQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRSLKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLV
KVNFAHFPRILISLHSLCLRRNKVAIVVSSLDWVWNLEKMDLSGNEIYMEPHVFETVPHLQSLQLDNRITYIE
PRIILNSWKSITSITLAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEP
SGHLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSFLIVVL
VLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVIINEYGSCTCHQOPAR
ECEV

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FIGURE 159

CAGAGAGGAGGCTTTGGGAATTGTCCAGCAGAAACAGAGAAGTCTGAGGTGGTGTCAAGACA
AAAG**ATG**CTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCAGAGTCT
CTTCTTGACAATCTTGGCAATGACCTAAGCAATGTGCTGGATAAGCTGGAACCTGTTCTTCA
CGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTGAAGGTCGACC
TAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCCCAGGAAGCTGAG
AAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAATAACACGGACATTTTTGGGTGAA
AATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGATGATGGCAAAGGCCTTA
ACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCCATCATTGGCCAGATTATC
AACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATTGAACTGATCCCCAGACACA
CCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCAACCAGCATCTCACTTTCCTTGC
TGGACAAACACAGCCAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGC
ACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCACTGATCCGCATCTTCATCCACTCCCT
GGATGTGAATGTCATTCAGCAGGTCGTCGATAATCCTCAGCACAAAACCCAGCTGCAAACCC
TCATC**TGA**AGAGGACGAATGAGGAGGACCACTGTGGTGCATGCTGATTGGTTCCCAGTGGCT
TGCCCCACCCCTTATAGCATCTCCCTCCAGGAAGCTGCTGCCACCACCTAACCAGCGTGAA
AGCCTGAGTCCCACCAGAAGGACCTTCCAGATAACCCCTTCTCCTCACAGTCAGAACAGCAG
CCTCTACACATGTTGTCCTGCCCCTGGCAATAAAGGCCCATTTCTGCACCCTTAA

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FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59622
><subunit 1 of 1, 249 aa, 1 stop
><MW: 27011, pI: 5.48, NX(S/T): 2
MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLV
DLGVLOKSSAWQLAKQKAQEAELNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDG
KGLNLSFPVTANVTAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS
ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ
HKTQLQTLI
```

Important features:**Signal peptide:**

Amino acids 1-15

N-glycosylation sites:

Amino acids 124-128;132-136

N-myristoylation sites:

Amino acids 12-18;16-22;26-32;101-107;122-128;141-147

Leucine zipper pattern:

Amino acids 44-66

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FIGURE 161

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGGACCAACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGG
GTGCTTGTGGCCTCCTATAACCACTTCTGCTCCTCGGACCTGTGCAATACTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTACAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGGCCTTCCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGAAGTGGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCTTTCA

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FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLM
LIESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLW
APQPPADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRRLRGGGIFSNLRVQGCM
PQPGCNLLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEV
GQVCQETLLLLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLN
SASSSSVLLNSLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLG
GGLSTKMSIQGCVAQPSSFLLNHTRQIGIFSAREKRQVQPPASQHEGGGAEGLESITWGV
GLALAPALWWGVVCPSC
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domain:

Amino acids 243-260

N-glycosylation sites:

Amino acids 46-50;189-193;382-386

Glycosaminoglycan attachment sites:

Amino acids 51-55;359-363

N-myristoylation sites:

Amino acids 54-60;75-81;141-147;154-160;168-174;169-175;
198-204;254-260;261-267;269-275;284-290;333-339
347-353;360-366;361-367;388-394;408-414;419-425

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FIGURE 163

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTGAGAAGAGCCAC
AGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTTCGAGGAGCTTCTGCATTGCTGGTT
CTGTTCTTGCAGCTTTTCTGCCCCCGCCGAGTGATACCCAGGACCCAGCCATGGTGCAATTACATCTACCAGCG
CTTTCGAGTCTTGGAGCAAGGGCTGGAAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCGAAGAGT
TCTCAAAAAATATATCTGTCTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAAGTGGGTAAAC
TTGGCACTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTGACGAGTGCAT
CGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAAGATCCGGACTCTGC
TGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAATAGTGAAGAAGATGATGGACACACAT
GGCTCTTGGATGAAAGATGCTGTCTATAACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGT
TTGGGAATTTGCAAACATACGGGCATTCTGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACAC
TTTCCTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTTCTAATGAG
ATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCAGGAGGGGTAGGCCGAGCAT
GGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCTCTGGGCCATCCACTCTG
GGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGAT
ACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATTCTCTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGG
GGGCCAGGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGGCCAACT
TGTTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCCTGG
AATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAAATGCAATTACAGCTGT
GAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGCCCCTTCACAATATAGTATCC
CTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAG
GTATCTTCCAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAACCTC
CTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTGTTTTACTGCTCCCCAGCATTTAC
TGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCTAATATTCACCACTGGCTTTTCTCT
CCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTTTCAAATGTCTATTGATATTCTCCCATTTTCACTGCCCCA
AAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGT
CTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCACCA
CACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTCTTCCACTAAGCTT
GGTAGATGTAATAATAAAGTGAAAAATTTAATATTTGAATATCGCTTCCAGGTGTGGAGTGTGTCACATCAT
TGAATTCCTCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCAATTCTAGAGTTTAGGTGAGTAACA
CAATTACAAAGTGAAAGATACAGCTAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCAAGGAAGCATCA
AATACGTATGTTGTTACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC
TTTAGCCAGTTTTCTGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTC
TAAGGGTGAGGACCCCAACTTAGCCTCCTCTGTCTTGTCTGCTCTGTTCTCTTTCTGCTTTAAATTCA
ATAAAGTGACACTGAGCAAAAAAAAAAAAAA

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FIGURE 164

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEFKSNISVMLGRC
QTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLLQEAEEEKKIRTLLNASCDNMLMGI
KSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTVWEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYK
GFLFFHNQATSNEIIKYNLQKRTVEDRMLLPGGVGRALVYQHSPTIYIDLAVDEHGLWAIHSGPGTHSHLVLT
IEPGTLGVEHSWDTPCRSQDAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFPPKRPRSHSM
IHYNPRDKQLYAWNENQIIYKLQTKRKLPLK

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FIGURE 165

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGCAGTGTGTTTGGC
TTCACCCCAAGTGACCAATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTCCTAGTAAGTGTGTCTGACTGTG
CTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTT
CGAGGGCTGCGGATGTGCACCCCGCTGGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTT
CTTCAGGAAACGCAAGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGT
ACCGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCTTTT
CCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGACTCTCCAGTCCCTACACTGACT
ACCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATACCTCCCATCATGACATGGTCCCCAG
GCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGC
TGCCAGAGAGGTGGTAAATGGCAGAAAGGACATCCCCCTCCCCTCCCAGGTGACCTGCTCTTCTTCTGGGC
CCTGCCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGTGCATTGCT
CAGAGTCCCAGGTCTTGGCCTGACCCCTCAGGCCCTTACGCTGAGGTCTGTGAGGACCAATTTGTGGGTAGTTCA
TCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTTCCCAGAGGGCAGCAGAC
AGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCT
GTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCAGAATTGTCTATGCCTCTGAGGCCCCCTCTTACCACACTTT
ACCAGTTAACCCTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAAAATGCAAATGGTGGTGGTTCAATCTAAT
CTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCTTAAACAACCTCTTCCAAGGATCAGCCCTGAGAGC
AGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGCAGGGCAGGG
GCTGAAAGGGGCACTGATTGAGACCAGGGAGGCAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAA
CTGAAAAAA

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FIGURE 166

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRK
HHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Important feratures:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 167

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGGTGTGGAGCCC
TCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTTATGGCAAGAGCTCTACTCGTGCGG
TGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTG
CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCT
AACAGTGACCTGGAATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCT
TCCAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCCATC
CTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCACCTGATGTTGATGG
GGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCTGAGATCCACTTCTGGCTCTGGCCA
TTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATTGTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGA
TGGGCCGAAAGAGCTCATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGT
CTCTGTTTATTTAGAAGACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTA
GTATTTCTTGAAGTTAATGGAACTTTTCTTGGCTTTTCCAGTTGTGACCCGTTTTCCAACCAAGTTCTGCAGC
ATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATATCACCAGTCATACACAGC
CTCATTATTAAGGTCTTATTTAATTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAG
CTACATTTTTGCCCCTTAAGACACTACTTACAGTGTATGACTTGATACACATATATTGGTATCAAAGGGGATA
AAAGCCAATTTGTCTGTTACATTTCTTTTACGATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGT
TTACTCTCTTTCTTCCACATTCTCAATTTAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAAACAGTAAA
TCCTAAATTCAAACGTGTTAAATGACATTTTTATTTTATGTCTCTCCTTAACTATGAGACACATCTGTTTTAC
TGAATTTCTTTCAATATTCCAGGTGATAGATTTTTGTGC

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FIGURE 168

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTWNFRPLDGGPEQ
FVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILWKLQFDDNGTYTCQVKNPPDVG VIGEIRLSVVHTVRF
SEIHFLALAIGSACALMIIIVVVL FQHYRKKRWAERAHKVVEIKSKEEERLNQEKKVSVYLEDTD

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FIGURE 169

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTTATCTGA
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
AGTTCCGTCGCGCTTGTGAAAGCCCCACCGAGAAATTAAGTCCGTTATCGTCATGTTCACTGCT
CTCCAACCTGCATAGACAGTGTGTGCGTTTGCAAGCAAGCTGATGAAGAATTCAGATCCTGGC
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTGGCATGGTGGATTTTTG
ATGAAGGCTCTGATGTATTTTCTGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGC
TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTTGGCTGTTATTGGTGGACTTGTGTAT
CTTCGAAGAAGTAATATGGAATTTCTCTTAAATAAACTGGATGGGCTTTTGCAGCTTTGTG
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTG
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG
TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
GACTTGTGTGATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTTCTGATGAGTTAAAAAGGTCCAGAGATATATAGACACTGGAGTACTGGAA
ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAAACTACTTTAGTTAACTTGGTCATCTGAT
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTCAIGTGGTCTTCTGAAAATG
GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
GATTTTCAAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAA
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 170

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLENKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

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FIGURE 171

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTTTCTGCATCTCC
AGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGATGCTGTGCCAGCCACACAAGAG
ATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTTGCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCC
AGACGTGTGGAAACTGCACCTTCAGAGTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATA
AACCAGAACTGCGACTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGCAGTGTGAGCTAAATGGAACATCAGGGG
AACGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGATGC
TGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCTTCATTCTGTGACCTGTCTGAGGCCCAC
CCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGACAGCATGAGATGCCGTGTGCTGATGG
GGGCCAGGACTCTGAACCTCCTGATGACCCCTATGGCCAACATCAACCGGCACCACCCAAGGCTGGCTG
GGGAACCTTCACCCTTCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATC
ATAATAAATTTATGTACTTTATAAATGAAA

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FIGURE 172

MAPRGCI VAVFAIFCISRL LCSHGAPVAPMT P YIMLCQPHKRCGDKFYDPLQHCCYDDAVVFLARTQT CGNCTF
RVCFEQCCPWT FMVKLINQNCDSARTSDDR LCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 173

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCCGCCCGCTCCCCGGCACCAGAAGTTCCCTCT
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC
CACGCCGTATTCCTGTATGTCTGTCCCGAGGGGCGAGAAGCTCACCCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
CCATGGTGGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT
ACCCATCCTCCTCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCAAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACC
CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCCGAGCCCAGCAC
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTCCCATCCCTGGACCCTGTCCCTGACT
CTCCAAACTTTGAGGTCATCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCCTGTTCCAAGGATTTTGGGGTGCTGAG
ATTCTCCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCCGAGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:
amino acids 1-28

Transmembrane domain:
amino acids 190-216

FIGURE 175

[illegible]

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FIGURE 176

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLATLQEAATTQENV
AWRKNWMVGGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 177

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGGCCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCT
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCC**ATG**AGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGACGGGCACCGGGCTGCAGCACCTAC
CGAACCATCTATAGGACCGCTACCGCCGACGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCG**TGA**CTGCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCCTCTTCTCCTCCCCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG

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FIGURE 178

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

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FIGURE 179

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCATCACGGGATATGTT
GATAAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCTCCCGGGCCACAGCGAAGTG
GAAAGGTCCACAAGGACAGGATTTGTCCACAGATCCAGGACAAACAGAGACATGCATGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACCTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCCTGGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG
GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCA
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

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FIGURE 180

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELEDWRKKGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTFFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

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FIGURE 181

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCAACGAGGAGAAGA
TGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGG
CGGCCTCGCCCTGTTGTGCTGCGCCGCGCGCGCGCGCGCGCTCGCCTCAGCCGCTCGGCGGGGAATGTCACCG
GTGGCGGCGGGCCGCGGGGCAGGTGGACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTC
CCTAGGGCGACGGCTCCACGCGCCAGGCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGC
TGCGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTCCACCACCTTTC
AGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCCGACC
AGACCCGCGCGGACCACCCCTTTCGACGACCCTGGCCCGGCGCGGACCACCCCTGTAGCGACCACCGTACCGGC
GCCCACGACTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTG
CCACCGAGGCCCCCTCTTCGCCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAAT
CGCTGCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGA
GGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATA
CGTGCAACAGGTAAGCAACAGAGGGTGGAAGTGAAGTTTATTTTATTTTAGCAAGGGAAAAAAAAGGCTGCTA
CTCTCAAGGACCATACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTA
TTCTCTTACTTTATATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAG
CACTAGAGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAATAAATCT
GCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATACCA
TTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTAATCAAAATTTCTACATTTGTTTCTTTGGACA
TCTAAAGCTTAACCTGGGGGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAG
TACATTTTTGAGACCAAAAGTAGATTAAGCAGGAATTATCTTTAACTATATGTTATTTGGAGGTAATTTAAT
CTAGTGGAATAATGTAAGTATCTAAGCATTTGCCTGTACTGCACTGAAAGTAATTATTCTTTGACCTTATG
TGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATG
ACAGGTTATACTCAGTGTAACCTGGGTATAACCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTGGGCAAG
TAATTTCTTTCACTGAGCTTGTTCCTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAATGC
CTAGCACATGTCACTCAATAAATCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACA
TGTTTTAAGAACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTATA
AATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAGAGGCTGGGCGCGGT
GGCTCAGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGA
GCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACCT
GTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGA
GATCGCGCACTGCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTVPATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 183

TGCGGCGCAGTG TAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGTCTCGGTGCCCCA
GGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCCCTGGTACGTGCTTGCGGTGGCC
TCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGA
AAACAACCTGCGGACGCTGCCTCTCAGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGC
GAAACTCCGGATGGGTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGA
GACTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCTGAC
GGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTTCCTGTCACAGTAGC
AGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGG
CGCCACAGGGTCCTGTGACCTCGGCCAGTGTCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCT
CAGAATAAAGCGATTCCACAGCA

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FIGURE 184

MGGLLLAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTLTPENNLRITLSS
QHGLGGCDQSVMDLIKRNKGWVFENPSIGVLELWVLATNFRDYAIIFTQLEFGDEPFNTVELYSLTETASQEAM
GLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20 \

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FIGURE 185

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACAGCAGCCAAGGA
ACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATCCTGCTTGCTCTGGCAACAGGGC
TTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAGTGCAGGCTCACTCCAGCCCTGGCAGGCAGCCCTG
TTCGAGAAGACGCGGCTACTCTGTGGGGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCT
CAAGCCCCGCTACATAGTTACCTGGGGCAGCACAACCTCCAGAAGGAGGAGGGGCTGTGAGCAGACCCGGACAG
CCACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGCTG
GTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCACGCTGTGTCACTGC
TGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCAGTCCAGCCCCCAGTTACGCCTGCCTCACACCTTGCGAT
GCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCGGCAACATCACAGACACCATGGTG
TGTGCCAGCGTGCAGGAAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTC
TCTTCAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCT
GCAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCATCACCC
TCCATTTCCACTTGGTGTTTGGTTCTGTTCCTCTGTTAATAAGAAACCCTAAGCCAAGACCCCTCTACGAACA
TTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCT
GGATTCAAATTCTGCCTTGAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCA
GCCCCAAAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 186

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAFRWLLTAHCLKPRYIVHLGQ
HNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI TWAVRPLTLSSRCVTAGTSCCLISGWG
STSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQD
PCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 187

GCTCAAGTGGCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG
ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTC¹CCCAAGGC
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAA²TTCCCTTTATACC
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
GGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
CTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT
TCCAGATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
CTACCAGCTGTTGGTACAGCTCAAGGACATGGGTGACCCAGGCCTCAGGACCACCGGCCACTG
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT
GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
AATTC³CCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTA⁴CTGAAGTGA⁵CTAGACTGTCAGCAGAGGATGCAGATGCCCCGGCTCCCCAATTCC
CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT
TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
GAAGGGACTTTTGGCCTGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
GAACCTCACTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTC⁶CCCATCAGTGCCCC
AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
CCCTAGTCAATGACTCAGAGGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
TTCACCCCTTGGTCCCAACCCACCGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
CCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTCGCTGCAAC
GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTGCGC
AGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTCACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCTGAAGGCG
ACTGTCTTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
TTTATGGA⁷CTGCCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGCCCAATAATAAAGCCCCA
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 188

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLEPIHLAE
NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFOVDPTSGSVTLGVLPRLAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDTE
GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHVQSVAKLVGPGPGGATATVTVLVERV
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISTRFSLVNDSEGWLCKIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTALHWVEPREHIIIPVVSHNAQMWQLLRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 189

[illegible]

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FIGURE 190

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRLTRIPSNLSSDT
QVLLLSQNNIAKTVDLQQLFNLTLDLDFSQNNFTNIKEVGLANLTQLTTLHLEENQITEMTDYCLQDLSNLQEL
YINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVGILDMNFKPLANLRSVL
AGMYLTDIPGNALVGLDSLESLSFYDNKLVKVPQALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINN
MGELVSVDRYALDNLPELTKLEATNNPKLSYIHLAFRSVPALSLMLNNAIYQKTVESLPNLREISIH
NPLRCDCVIHWINSNKTNIRFMEPLSMFCAMPPEYKGHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGTTVF
LDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNVQGADTRVATIKVNG
TLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPHITYTARVPVDVHEYNLTHLQPDY
EVCLTVSNIHQQTQKSCVNVTTKNAFAVDISDQETSTALAAMGSMFAVISLASIAVYFAKRFKRKNYHSLK
KYMQKTSSIPLNELYPPLINLWEGDSEKDKDGSADTKPTQVDTSRSYYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

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FIGURE 191

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

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FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 193

GAAGTAGAGGTGTTGTGCTGAGCGGCGCTCGGCGAACTGTGTGGACCGTCTGCTGGGACTCC
GGCCCTGCGTCCGCTCAGCCCCGTGGCCCCGCGCACCTACTGCC**ATGG**GAGACGCGGCCTCGT
CTCGGGGCCACCTGTTTGTGCTGGGCTTCAGTTTCCTGCTCCTCGTCATCTCTTCTGATGGACA
TAATGGGCTTGGAAAGGGTTTTGGAGATCATATTCATTGGAGGACACTGGAAGATGGGAAGA
AAGAAGCAGCTGCCAGTGGACTGCCCCTGATGGTGATTATTCATAAATCCTGGTGTGGAGCT
TGCAAAGCTCTAAAGCCCAAATTTGCAGAATCTACGGAAATTTCAGAACTCTCCCATAAATTT
TGTTATGGTAAATCTTGAGGATGAAGAGGAACCCAAAGATGAAGATTTACAGCCCTGACGGGG
GTTATATTCCACGAATCCTTTTTCTGGATCCCAGTGGCAAGGTGCATCCTGAAATCATCAAT
GAGAATGGAAACCCAGCTACAAGTATTTTTATGTCAGTGCCGAGCAAGTTGTTACAGGGGAT
GAAGGAAGCTCAGGAAAGGCTGACGGGTGATGCCTTCAGAAAGAAACATCTTGAAGATGAAT
TG**TAA**CATGAATGTGCCCCTTCTTTCATCAGAGTTAGTGTCTGGAAGGAAAGCAGCAGGGA
AGGGAATATTGAGGAATCATCTAGAACAATTAAGCCGACCAGGAAACCTCATTCCTACCTAC
ACTGGAAGGAGCGCTCTCACTGTGGAAGAGTTCTGCTAACAGAAGCTGGTCTGCATGTTTGT
GGATCCAGCGGAGAGTGGCAGACTTTCTTCTCCTTTTCCCTCTCACCTAAATGTCAACTTGT
CATTGAATGTAAAGAATGAAACCTTCTGACACAAA

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FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67300
><subunit 1 of 1, 172 aa, 1 stop
><MW: 19206, pI: 5.36, NX(S/T): 1
METRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHWRTLEDGKKEAAASGLPLMVI
IHKSWCGACKALKPKFAESTEISELSHNFVMVNLEDEEPPKDEDFSPDGGYIPRILFLDP
SGKVHPEIINENGNPSYKYFYVSAEQVVQGMKEAQRLTGD AFRKKHLEDEL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Thioredoxin family proteins:

Amino acids 58-75

N-myristoylation sites:

Amino acids 29-35;67-73;150-156

Amidation site:

Amino acid 45-49

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FIGURE 195

CGGCTCGAGTGCAGCTGTGGGGAGATTTCACTGCATTGCCTCCCCTGGGTGCTCTTCATCTTGATTGAAAGT
TGAGAGCAGCATGTTTTGCCCACTGAACTCATCCTGCTGCCAGTGTTACTGGATTATTCCTTGGGCCTGAATG
ACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGC
ACAGAAGACAAATGTATATTCAAGATAGACTGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCT
ATACTATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTAT
GCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGCCTC
AAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCAAAGAGCTCATGGT
CCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAGAGCACAGAAGTGAACACCGTGACCAAGGTAGAAT
GGATATTTTTCAGGACGGCGCGCAAGGAGGAGATTGTATTTTCGTTACTACCACAAACTCAGGATGTCTGTGGAG
TACTCCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCAT
CATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTC
AGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTG
GTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTGAT
ATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGA
CTAATCCAGAGATAAAAGAAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATA
ATTGTACGGGAGGTGATCGAGGAAGAAGAACCAAGTAAAAATCAGAGGCCACCTACATGACCATGCACCCAGT
TTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGC
AAGCCTTTTGAAGAAGAATGGAGAGTCCCTTCTCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGTCTCTGGGC
CACTCTACCAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAG
ATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATG
GACTTGGCCTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGAT
CAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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FIGURE 196

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGEHAKDEYVLYYY
SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPPEPKELMVHVG
GLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQ
GVRES DGGNYTCSIHLGNLVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVLLILIV
KKTCGNKSSVNSTVLVKN TKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPS
LRSDRNNSLEKKSGGGMPKTQQAF

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FIGURE 197

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTGCGGGCGGCCGGGACCACGGGGACTGGGA
CGAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCG
TGACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGC
CGGCCCTTCGCCGACGTCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCC
CTATTTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTA
CACTGACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGT
CCCCTTTGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGA
TATTGCAAAGCATTGCTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATA
ATTGGTTCTTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCA
AAAATCGTGACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAAT
TTAGCAACACTTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCT
CTGGAAAGCGTCCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 198

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ

Important features of the protein:**Transmembrane domain:**

Amino acids
11-29

N-glycosylation sites:

Amino acids
160-164;193-197;216-220

N-myristoylation sites:

Amino acids
3-9;7-13;69-75;97-103

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FIGURE 199

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACCT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCTACCTCTGGGA
TTGTCTTTGTCTCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGA**CGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTCTTTTGAAGTGGGATATTTAAATTCATTT
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTCACCCCTGGAAAAACAAATCATCTG
TTAACAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTTACACTCACATTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

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FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPHSHMARYSTSAPAISRGPSSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 201

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGTCTCCTTCTGCTC
TGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAAAAAAGTGGACTGCAGCATTTA
CAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACATACCTACCAGTTTGTGGTTCTGACTACATCACCT
ATGGGAATGAATGTCACTTGTGTACCGAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGT
TGCTAAATTCTCCATGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGAC
TGAGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAATGGA
GAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTTAACACGTCAATAA
AAAAATAATCTCCAGA

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FIGURE 202

MKITGGLLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNECHLCTESLKSN
GRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 203

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGGCTGCGGCGCTG
CTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCTCGTCGCTCAGCCCTATTTTCGG
CACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGTGCGGCCCGGAGGCTCCGTGGCGGGACCCCTGAGC
TGCTGGAGGGGACCTGCACCCCGGTGCAGCTGGTGCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAA
CAGATCCGCAAGCTGAGGCAGCTGCACGGGTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTAC
CGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGCTAG
TAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGGCCCTTTTCAGCCGT
GAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCATGGATAGCAGCGCCGCTTCTCTGCA
GGGGCTGTGGCAGCACTACCACCCTGGCTTGGCGCCGCCGACGTCGCAGATATGGAGTTTGGACCTCCAACAG
TTAATGATAAACTAATGAGATTTTTTGTACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCT
CTTTATCAGCTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCA
AGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAGTAGCCTTTTTCACCTGTTTCAATTTGACCTGGCAATTA
AAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAGAATATTTAAATGATCTG
AAACAATATTGGAAGAGGATATGGGTATACTATTAACAGTCGATCCAGCTGCACCTTGTTTTCAGGATATCTT
TCAGCACTTGGACAAAGCAGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCTCCAGTTTG
GTCATGCAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTAC
AATTACAAAAACAAATGCATCGGAAGTTCGGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGT
GCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAATGAAAAGGTGT
TACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAG
AGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGCTAACAGTACATCTGATGAAGTATGAGTAACTGAAGA
ACATTTTAAATCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAAATAGGTAGGCAATTCCTTGATTACAG
GAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATG
AAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGCC
CTGCAATGTTTACAGAAATGAAATCTTCTACTTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTT
ATAATAACACTTGAAAAGTGTGGAGTAACAAAATATCTCAGTTGGACCATCCTTAAGTTGATTGAACTGTCTA
GGAACCTTACAGATTGTTCTGCAGTTCTCTCTTCTTCTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATCAG
GAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAAC
AGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAAATATTTTGGTATTTAT
TTATGAAATATTTGAACATTTTTTCAATAATTCCTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTA
TTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACT
TTTTCACTCTGTCACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTGTGTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAATAAGAAAATTC
TTGTGACTTTAAAAAAA

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FIGURE 204

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLSGPEAPWRDPELL
EGTCTPVQLVALIRHGTRYPTVKQIRKLRLHGLLQARGSRDGGASSTGSRDLGAALADWPLWYADWMDGQOLVE
KGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMDSSAAFLQGLWQHYPGLPPPVDADMEFGPPTVN
DKLMRFFDHCEKFLTEVEKNATALYHVEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKG
VKSPWCDVFDIDDAKVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGH
AETLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLIQVLYHCENAKTPKEQFRVQMLLNEKVLP
LAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 205

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGG**TAGA**AAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRINDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:
amino acids 1-20

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FIGURE 207

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGCCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

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FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

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FIGURE 209

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTGGGGTGGTCTGTCTGCTCCTGGCATGCCCT
GCCACAGCCACTGGGCCCCAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTGCTGTGCGAGGCCGGCAGGT
GGGCGTGAAGGGCACAGACCGCCTTGTGAATGCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTG
ACCGGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGC
CTACAAGACGTGGAGAGCATGAACAGCAGCAGATTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGA
GGACTGCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGG
TCCATGGAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTG
GTCGTGGTTACAGTCCAGTACCGCCTTGGGGTCCCTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAA
CCAGGGCTTCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCA
ACTGTGTCACTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCA
GGGCTGTTCCACAGAGCCATCACACAGAGTGGGGTCACTACCACCCAGGGATCATGACTCTCACCCTTGGCC
CCTAGCTCAGAAAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAG
AGAAAGAAGGAGAAGAGCTGGTCCCTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCCTTGATGGCACT
GTCTTCCCCAAAAGCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAA
CAACCATGAGTTCAGCTGGCTCATCCCCAGGGGTGGGGTCTCTGGATACAATGGAGCAGATGAGCCGGGAGG
ACATGCTGGCCATCTCAACACCCGTCTTGACCACTCTGGATGTGCCCTGAGATGATGCCACCGTCATAGAT
GAATACCTAGGAAGCAACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTCT
CAATGTTCCACCGTCAGTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGC
ATCGACCCAGTTCTTTTGCAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTG
TTCGGAGGTCCCTTCTCATGGACGAGAGCTCCCGCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCT
AAGCCTCACCATGATGGCCCAGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTT
GGCCCCAATTCAACCAGGCGGAACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTCAGGGAG
GCCTGGATGCAGTCTCTGGTCAGAGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAA
GGCCCAGGAGACCTCTGAGGCCAGGCCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAG
TCCCAGCACGGCAGCCCGCCTCTCCCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCT
GTGACTGGAGTTATGCTCTTTTGAAATGTACAGGCCCGCCTCCACCTCTGGGGCATTGTACAAGTTCTTCCC
TCTCCCTGAAGTGCCCTTCTCTGCTTCTTCTGCTGGTAGGTTCTAGCACATTCCTCTAGCTTCTTGGAGGACTCAC
TCCCCAGSAAGCCTTCCCTGCCTTCTCTGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCC
GAGGCTAGCACCGTGTCTGTGTCTGTCTCCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCAC
TCTGTCAACCCACACAGGATCGGGTGGGACCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGA
ATATGGGAATGGCAGCTGCTGAACCTGAACCCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGAC
ATTGTCCACCCTGGCCAGAAGGGTGCATGCCAATGGCAGAGACCTGGGATGGGAGAAGTCTTGGGGCGCCAGGG
GATCCAGCCTAGAGCAGACCTTAGCCCCGACTAAGGCCTCAGACTAGGGCGGGAGGGGTCTCTCTCTCTGCTG
TGCCCACTGCTGGCCCCCTGCACAAGACAACAGAATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCCTCAC
CAATTCCAGCCCCCTGACCCCTCAGGACGCTGGATGCCAGCTCCAGCCCCAGTGCCGGGTCTCCCTCCCTTCCT
GGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAGAGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGG
CATCTGGACCAGGGCATCCGTGGGGCTATTGTACAGAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGG
TGAAAAGCACCAGAGGTTTTTTCAGATGGAAGTGAGAGGTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTG
CTCTCCCTGCCGCTCTGCCTGGGCTCCCACTTTGGCAGCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGT
AGGAGCCCCCTTCTGGGCTGGCCAAGGCCGAGCCAGCTCCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGG
CGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAGAGTGAGTTCGGGTGGGCGTGGGCTCGGCGGGG
CCCACTCAGAGCAGCTGGCCGGCCCCAGGCACTGAGGGCTTAGCACCTGGGCCAGCAGCTGCTGTGCTCGATT
TCTCGCTGGGCTTAGCTGCCTCCCCGCGGGGAGGGCTCGGGACCTGCAGCCCTCCATGCCTGACCCCTCCCC
CACCCCCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAGCGCCGCCCCCTGCTCCACAGCGCCAGTCCC
ATCGACCACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGACTGGCAGGCAGCTCCACCTGCTGCCCCAGT
GCTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGGGACTTGAGAACTTTATGTCTAGCTAA
GGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCTGTGT
CTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCTACTCTGGTGGGACTTGAGAACTTT
GTGTCCACACTCTGTATCTAGCTAATCTAGTGGGATGTGGAGAACCTTTGTGTCTAGCTCAGGGATCGTAAAC
GCACCAATCAGCACCTGTCAAAACAGACCACTTGACTCTCTGTAAATGGACCAATCAGCAGGATGTGGGTGG
GGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCCCTCGGGTCCCTCCACGCGCT
GGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTGCTACTGCCAAAA

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FIGURE 210

MERAVRVESGVLVGVCLLLPATATGPEVAQPEVDTTLGRVRGRQVGKGTDRLVNVFLGIPFAQPPLGPDR
FSAPHPAQFWEGRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLVNLVYSPAIEVPAGSGRPVMVWH
GGALITGAATSYDGSALAAAGDVVVVTQYRLGVLGFFSTGDEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNC
VTVFGGSAGGSIISGLVLSFVAAGLFHRAITQSGVITTPGIIDSHFWPLAQKIANLACSSSSPAEMVQCLQQK
EGEELVLSKKLKNTIYPLTVDGTVFPKSPKELLKEKPFHSPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDM
LAISTPVLTSLDVPPPEMMPTVIDEYLGNSNSDAQKCAAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEFOHR
PSSFAKIKPAWVKADHGAEGAFVFGGPFLLMDESSRLAFPEATEEEKQLSLTMMAQWTHFARTGDPNSKALPPWP
QFNQAEQYLEINPVPRAGQKFRQAWMQFWSETLPSKIQQWHQKQKNRKAQEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161, 162-168, 217-223,
227-233, 228-234, 232-238, 262-268, 357-363, 461-467**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 211

AACTTCTAC**ATG**GGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACAC
CATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCC
GGGAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTG
GTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAG
GGTTTTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCAGTAGCC
ACCAGCCACCTGTGGCCGTTGAGTGCTTGAAAT**TGA**GGAACTGAGAAAATTAATTTCTCATGT
ATTTTCTCATTTATTTATTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGA
TATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACA
TCAAACATTTATTTTTTTATTCTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGC
AGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTC
CACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTT
TAGTAGAGACGGGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCTGGCCTCAAACAAT
CCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAA
ACATTTATCTTTTCTTTGTGTTGGGAACCTTGAAATTATACAATGAATTATTGTTAACTGTC
ATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTAC
CAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCA
TTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCA
ATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATG
TTGCTGCAAAATGACAGGATTTGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

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FIGURE 212

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSC
QPVKGHGTLGESPMFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 213

AGGGCCCGCGGGTGGAGAGAGCGACGCCCGAGGGGATGGCGGCAGCGTCCCGGAGCGCCTCT
GGCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGCCGCTCCGGCGTCTT
CCAGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCG
AGCCCGGCTGCCGGACTTTCTTCCGCGTCTGCCCTTAAGCACTTCCAGGCGGTGCTCTCGCCC
GGACCCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCG
GGACGACAGTAGCGGCGGGGGGCGCAACCTCTCCAACCTGCCCTTCAATTTACCTGGCCGG
GTACCTTCTCGCTCATCATCGAAGCTTGGCAGCGGCCAGGAGACGACCTGCGGCCAGAGGCC
TTGCCACCAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGAGAA
CTGGTTATTGGATGAGCAAACCAGCACCTCACAAGGCTGCGTACTCTTACCGGGTCATCT
GCAGTGACAACTACTATGGAGACAACTGCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTC
GGCCACTATGTGTGCCAGCCAGATGGCAACTTGTCTGCTGCCCGGTGGACTGGGGAATA
TTGCCAACAGCCTATCTGTCTTTCGGGCTGTGATGAACAGAATGGCTACTGCAGCAAGCCAG
CAGAGTGCCTCTGCCGCCAGGCTGGCAGGGCGCGGTGTGTAACGAATGCATCCCCACAAT
GGCTGTGCGCCACGGCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGG
CCTGTTTTGTGACCAAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAA
CGTGCTCCAACAGTGGGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTG
GACTGTGAGCTGGAGCTCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAA
GGACCAGGAGGATGGCTACCACTGCCTGTGCTCTCCGGGCTACTATGGCCTGCAGTGTGAAC
ACAGCACCTTGAGCTGCGCCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAAC
CAGGGGGCCAACTATGCTTGTGAATGTCCCCCACTTCACCGGCTCCAACCTGCGAGAAGAA
AGTGGACAGGTGCACCAGCAACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAA
GCCGCATGTGCCGCTGCCGTCCTGGATTACGGGCACCTACTGTGAACTCCACGTCAGCGAC
TGTGCCCGTAACCCCTTGCGCCACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTG
CACCTGCCCTGCCGGCTTCTCTGGCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTG
CCTCGAGTCCCTGCTTCAACAGGGCCACCTGCTACACCGACCTCTCCACAGACACCTTTGTG
TGCAACTGCCCTTATGGCTTTGTGGGCAGCCGCTGCGAGTTCCCGTGGGCTTGCCGCCAG
CTTCCCCCTGGGTGGCCGTCTCGCTGGGTGTGGGGCTGGCAGTGTGCTGGTACTGCTGGGCA
TGGTGGCAGTGGCTGTGCGGCAGCTGCGGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCC
ATGAACAACTTGTGCGACTTCCAGAAGGACAACCTGATTCTGCCGCCAGCTTAAAAACAC
AAACCAGAAGAAGGAGCTGGAAGTGGACTGTGGCCTGGACAAGTCCAACCTGTGGCAAACAGC
AAAACCACACATTGGACTATAATCTGGCCCCAGGGCCCCCTGGGGCGGGGGACCATGCCAGGA
AAGTTTCCCCACAGTGACAAGAGCTTAGGAGAGAAGGCGCCACTGCGGTTACACAGTGAAAA
GCCAGAGTGTGCGATATCAGCGATATGCTCCCCAGGGACTCCATGTACCAGTCTGTGTGTT
TGATATCAGAGGAGAGGAATGAATGTGTGTCATTGCCACGGAGGTATTAAGGCAGGAGCCTACCT
GGACATCCCTGCTCAGCCCCGCGGCTGGACCTTCCTTCTGCATTGTTTACA

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FIGURE 214

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCPEPGCRTFFRVCL
 KHFAQVVSPPGCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLLIEAWHA
 PGDDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQSTLTTRLRYSYRVICSDNYYGDNCNR
 LCKKRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGR
 LCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSCKNGATCSNSGQORSYTC
 TCRPGYTGVDCLELSECDNPNCRNGGSCDKQEDGYHCLCPPGGYYGLHCEHSTLSCADSPCF
 NGGSCRERNQGANACECPNFTGNSNCEKKVDRCTSNPCANGGQCLNRGPPSRMCRCPGFTG
 TYCELHVSDCARNPCAHHGGTCHDLENGLMCTCPAGFSGRRCVVRTSIDACASSPCFNRTCY
 TDLSTDTFVCNCPYGFVGSRCFFVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLR
 RPDDGSREAMNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQONHTLDYNLAPG
 PLGRGTMPGKFPHSDKSLGEKAPLRHLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIA
 TEV

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 530-552

N-glycosylation sites.

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

Glycosaminoglycan attachment site.

amino acids 96-100

Tyrosine kinase phosphorylation site.

amino acids 340-347

N-myristoylation sites.amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

Aspartic acid and asparagine hydroxylation site.

amino acids 339-351

EGF-like domain cysteine pattern signature.amino acids 173-185, 206-218, 239-251, 270-282, 310-322,
348-360, 388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394,
411-432, 449-470

FIGURE 215

[illegible]

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FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFAFSLISITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCIVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302**Myelin P0 protein.**

amino acids 96-125

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FIGURE 217

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTTCACTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
ATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
AGCAGGTGATGTATTTTTTATACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGGCT
AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAA

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FIGURE 218

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGN
IDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSTLT
IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

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FIGURE 219

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCC
GCGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCTGAGCCTCGGGCTCCGGCCCGGAC
CTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGAT
GGCTTTAAAGTGCTACTAGAACAAAGAGAAAAACGTTTTTCACTCTTTTAGTATTACTAGGCT
ATTTGTCATGTAAAGTGAAGTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGG
TCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGG
CTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACT
GGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCA
AATTGTTTCAGCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGAC
GAACTTGTGCGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACG
AACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCACGG
GACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGTGGCCCTGCTCAT
CCTCTGTGTATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGT
CGCAGGACATTCAGTACAACGGCTCTGAGCTGTCTGTGTTTACAGACCTCAGCTCCACGAA
TATGCCCACAGAGCCTGCTGCCAGTGGCGCGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGT
CTTGCTCCCATCCATGTGCTGTGAGGAGGCGTGCAGCCCCAACCCGGCGACTCTTGGTTGTG
GGGTGCATCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGAGATGGTGCCG
ACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGGCCTCTGAT
GCAGAATCCCATGGGTGGTGACAACATCTCTTTTGTGACTCTTATCCTGAACCTCACTGGAG
AAGACATTCATTCTCTCAATCCAGAAGTGAAGCTCAACGTCTTTGGATTCAAATAGCAGT
CAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTAC
TGATTTATCTAGATATAACAACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTA
TGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTATCCACCCAGCCACTCAGACGTCCCTC
CAGGAAGCTTAAAGAACCTGCTTCTTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTA
CTCCTTTGTTAGGCTTATGGACTGAGCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATA
AATCTGAACCAAACCTGACGGCATTGTAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGC
TGTAAGCTGAAACCTCAATGAATAACAAGAAAAGACTCCAGGCCGACTCATGATACTCTGCA
TCTTTCCTACATGAGAAGCTTCTCTGCCACAAAAGTGAAGTCAAGACTGATGGGTTGAGCT
GGCAGCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATGCTTATTTTCAT
GGTGATTGTGGTTTTACAAGACTGAAGACCAGAGTATACTTTTTCTTCCAGAAATAATTT
CATACCGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAGT
GAGTGTCTTATTTGAGAAGGACACTTTTTCATCATCTAAACTGATTTCGCATAGGTGGTTAG
AATGGCCCTCATATTGCCTGCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAATCAGAG
GAATCAGACAGAGGAGGATAGCTCTTCCAGAATCCACACTTCTGACCTCAGCCTCGGTCTC
ATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGGAATGTGGTTCGAGAAAGGGCAGC
CCATTGCCCAGAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGGCATATTTATATG
AAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCCTCTGCCTGAGCTTAGAAGGTTAT
AGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGTATCTTATACTAAAGGC
TTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGTAGCCTTCCGTGAGAACACACC
ACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTTGGATGAAGCAGCTGTAAGT
CCCTAGTGTAGTTTGACCAGGACATTGTCTGTCTCCTTCCAATTGTGTAAGATTAGTTAGCA
CATCATCTCCTACTTTAGCCATCCGGTGTGGAATTTAAGAGGACGGTGTCTTCTTCTATTAA
AGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAGCTAAGACAGAAATTAAC
CCCGTTCAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTTTATGCCCTGGAGAAGA
CCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGTTTCGAGGGTACTATGA
TATTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTTAACTGAATATTAA
AATGTATCTGTCTTTCCT

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FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHREFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLLPSMCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDL SRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLOEA
```

Important features of the protein:**Signal peptide:**

Amino acids
1-25

Transmembrane domain:

Amino acids
169-192

N-glycosylation sites:

Amino acids
105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids
200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids
207-214

N-myristoylation sites:

Amino acids
55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids
259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids
89-96

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FIGURE 221

[illegible]

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FIGURE 222

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQS
KDYYAYRLGHILNSWKEQVESKTVFSMELLGLRTRCGKFEDDIDNCHFQESTELNNTFTCF
TISTRPWMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

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FIGURE 223

AATCGGCTGATTCTGCATCTGGAACTGCCTTCATCTTGAAAGAAAAGCTCCAGGTCCCT
TCTCCAGCCACCCAGCCCCAAGATGGTGATGCTGCTGCTGCTGCTTTCCGCACTGGCTGG
CCTCTTCGGTGCGGCAGAGGGACAAGCATTTCATCTTGGGAAGTGCCCCAATCCTCCGGT
GCAGGAGAATTTTGACGTGAATAAGTATCTCGGAAGATGGTACGAAATTGAGAAGATCCC
AACAACCTTTGAGAATGGACGCTGCATCCAGGCCAACTACTCACTAATGGAAAACGGAAA
GATCAAAGTGTTAAACCAGGAGTTGAGAGCTGATGGAACTGTGAATCAAATCGAAGGTGA
AGCCACCCCAAGTTAACCTCACAGAGCCTGCCAAGCTGGAAGTTAAGTTTTCCTGGTTTAT
GCCATCGGCACCGTACTGGATCCTGGCCACCGACTATGAGAATATGCCCTCGTGTATTCT
CTGTACCTGCATCATCCAACCTTTTTCACGTGGATTTTGCTTGGATCTTGGCAAGAAACCC
TAATCTCCCTCCAGAAACAGTGGACTCTCTAAAAAATATCCTGACTTCTAATAACATTGA
TGTCAAGAAAATGACGGTCACAGACCAGGTGAACTGCCCCAAGCTCTCGTAAACCAGGTTCT
TACAGGGAGGCTGCACCCACTCCATGTTACTTCTGCTTCGCTTTCCCTACCCACCCCC
CCCCCATAAAGACAAACCAATCAACCACGACAAAGGAAGTTGACCTGAACATGTAACCAT
GCCCTACCTGTTACCTTGCTAGCTGCAAATAAACTTGTTGCTGACCTGCTGTGCTCGC
AAAAAA

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FIGURE 224

MVMLLLLLSALAGLFGAAEGQAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTTFENG
RCIQANYSLMENGKIKVLNQELRADGTVNQIEGEATPVNLTEPAKLEVKFSWFMPSPAY
WILATDYENYALVYSCTCIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKM
TVTDQVNCPKLS

Signal sequence

1-16

N-glycosylation site.

65-68

98-101

cAMP- and cGMP-dependent protein kinase phosphorylation site.

175-178

N-myristoylation site.

13-18

16-21

Lipocalin proteins.

36-47

120-130

Lipocalin / cytosolic fatty-acid binding proteins

41-185

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FIGURE 225

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGACGTACGGCCGTCACCCGCACCGCTG
CCTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGG
GCGTGGCCGAGGCCGGGGTGACCCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAA
TTCAGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCA
AAAAAGGACTCACCTCCCAAAAATTCGCTGAAGGTTGATGAGCTTTCACCTACTCAGTTCC
TGAGGGTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGC
TCCGACACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTACTCCCAAACTAAGCCC
AAGATGCAAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCC
TGGATTTTTTCCGAGACTTGGTGTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTA
GAGGTTCAAAAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTC
TATTATCCACAACAAGCCATCGTGTTTGCCAGGTCAGTGGGAGAGATTATATGACTGGGG
TTTACGAGGATATATAGTCATAGAAGATTTGTGGAAGGAGAACTTTCAAAGCCAGGAAATG
TGAAGAATTCACCTGGAACCTAAGTAGAAAACTCCATGCTCTGCCATCTTAATCAGTTATAGG
TAAACATTGGAACTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAG
TATTGAATGTATTAAATGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTT
CTGTGAAATCATCCTACAAGCAAACCTAACCTGGAATCCCTTCACCTAGAGATAATGTACAAG
CCTTAGAACTCCTCATTCTCATGTTGCTATTTATGTACCTAATTAAACCCAAGTTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 226

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEE
SISQLRHYPEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIG
LLLARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQ
KPGNVKNSPGTK

Important features:

Signal peptide:

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195

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FIGURE 227

CACCGGAGGGCAGCGAGCTGACGGAGCTGCGCTGCGTTGCGCTCGTTCGCTCGCGCCCTCC
ACTGGAGCTGTTGCGCGCTCCCGGCTCCACCGCAGCCCCACCGGCAGAGGAGTCGCTACCA
GCGCCCAGTGCGCTCTGTGAGTCCGCAAACTCCTTGCCGCCCCGCCCCGGGCTGGGCACCAA
TACCAGGCTACC**ATGGT**CTACAAGACTCTCTTCGCTCTTTGCATCTTAAGTGCAGGATGGAG
GGTACAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCAC
CGACCACCATCTGGACTAGCTCTCCACAAAACACTGATGCAGACACTGCCTCCCCATCCAAC
GGCACTCACAACAACTCGGTGCTCCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAA
GAACATTTCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTGAATTGGGAAGGCA
CAAACACAGACCCCTCACCTTCTGGGTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACC
ACGTTGGAGGAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGCAGTC
CGCTGCTGAGCCTCCACACTCATCTCCCTCAAGCTCCAGCCTCATCACCTCATCCCTAT
CAACCTCACACCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACC
AGCACCCAACCCACTGGAGCTCCAAGTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGA
CCACACACCCACTTCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAA
CTGTGTGTCAGGCAAAGTGATGTGTGAGCTCATAGACATGGAGACCACCACCTTTCCCAGG
GTGATCATGCAGGAAGTAGAACATGCATTAAGTTCAGGCAGCATCGCCGCCATTACCGTGAC
AGTCATTGCCGTGGTGTCTGCTGGTGTGTTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCTC
CCTATGGAAGACTTTTGGACGACCATGACTACGGGTCTGGGGAAACTACAACAACCCCTCTG
TACGATGACTCC**TAA**CAATGGAATATGGCCTGGGATGAGGATTAAGTGTCTTTATTATATAA
GTGCTTATCCAGTAGAATTAATAAGTACCTGATGCGCATTGAACGACAATCTTAAGCCCTGT
TTTGTTGGTATGGTTGTTTTGTTTTTCCCTCCCTCTCCTCTGGCTGCTACAACCTCCCCTTTC
TGGTACAAGAAGAACCATTCTTTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCA
GCCTTGCAACCAGCCAGGCCAGACCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCAC
TTTGAGAAGGATCGAGGAGGAGGATTTGGGTTGTTTTGTTAGGGGTTACTTTTCAGGGGAACA
TTTCATTTGTGTTATTTCTTAACTTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGA
AAGGAAATGAGCTCTACGAGGATTTACCTTGCATGGGAGAGAGCAGGGTTTTCTCAGATTC
CTTTTTAATCTCTATTTATCTGGTTGTTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGC
TGGAAGCAGCTTCTTAGCTGCCTAATTAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGG
GGCCAGCAGGTCACGGGGCAGAATCTCTCAGGTTGCTGTGGGATCTCAGTGTGCCCTACCT
GTTCTCCCCTCCAGGCCACCTGTCTCTGTAAAGGATGTCTGCTCTGTTCAAAGGCAGCTGG
GATCCCAGCCACAAGTGATCAGCAGAGTTGCATTTCCAAAGAAAAAGGCTATGAGATGAGC
TGAGTTATAGAGAGAAAGGGAGAGGCATGTACGGTGTGGGGAAGTGGAAGAGAAGCTGGCGG
GGGAGAAGGAGGCTAACCTGCACTGAGTACTTCATTAGGACAAGTGAGAATCAGCTATTGAT
AATGGCCAGAGATATCCACAGCTTGAGAGAGCCAGAGACTGTTTGCTTTATACCCACACAG
CAACTGGTCCACTGCTTTACTGTCTGTTGGATAATGGCTGTAAAATGTTTAAAAAC

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FIGURE 228

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHN
NSVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEE
HSSGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQP
TGAPTAPESPTEESSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELDMETTTTTFPRVIMQ
EVEHALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLDDHDYGSWGNYNPLYDDS

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 258-278

N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

Casein kinase II phosphorylation sites.

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

Tyrosine kinase phosphorylation site.

amino acids 289-296

N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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FIGURE 229

CTCCTGCACTAGGCTCTCAGCCAGGGATGATGCGCTGCTGCCGCCGCCGCTGCTGCTGCCGG
CAACCACCCCATGCCCTGAGGCCGTTGCTGTTGCTGCCCCCTCGTCCTTTTACCTCCCCTGGC
AGCAGCTGCAGCGGGCCCAAACCGATGTGACACCATATACCAGGGCTTCGCCGAGTGTCTCA
TCCGCTTGGGGGACAGCATGGGCCGCGGAGGCGAGCTGGAGACCATCTGCAGGTCTTGGAAT
GACTTCCATGCCTGTGCCTCTCAGGTCTGTGTCAGGCTGTCCGGAGGAGGCAGCTGCAGTGTG
GGAATCACTACAGCAAGAAGCTCGCCAGGCCCCCCCGTCCGAATAACTTGCACACTCTGTGCG
GTGCCCCGGTGCATGTTTCGGGAGCGCGGCACAGGCTCCGAAACCAACCAGGAGACGCTGCGG
GCTACAGCGCCTGCACTCCCCATGGCCCCTGCGCCCCCACTGCTGGCGGGCTGCTCTGGCTCTG
GCCTACCTCCTGAGGCCTCTGGCCTAGCTTGTTGGGTTGGGTAGCAGCGCCCGTACCTCCAG
CCCTGCTCTGGCGGTGGTTGTCCAGGCTCTGCAGAGCGCAGCAGGGCTTTTCATTAAAGGTA
TTTATATTTGTA

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92265
><subunit 1 of 1, 165 aa, 1 stop
><MW: 17786, pI: 8.43, NX(S/T): 0
MMRCCRRRCCCRQPPHALRPLLLLPLVLLPPLAAAAAGPNRCDTIYQGFAECLIRLGDSM
GRGGELETICRSWNDFHACASQVLSGCPPEAAAVWESLQQEARQAPRPNNLHTLCGAPVH
VRERGTGSETNQETLRATAPALPMAPAPPLLAALALAYLLRPLA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Transmembrane domain:

Amino acids 141-157

N-myristoylation site:

Amino acids 127-133

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 77-88

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FIGURE 231

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACCTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAAAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAA

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FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFRHWLVTDIKGADLK
KGKIQGQELSAHQAPSPPAHSGFHRHQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

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FIGURE 233

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

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FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:
amino acids 1-18

N-glycosylation sites.
amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 102-106

N-myristoylation site.
amino acids 24-30

Actinin-type actin-binding domain signature 1.
amino acids 159-169

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FIGURE 235

GCCCCGGGCGGCTGCCCTTGGGTGCTCCCTTCCCTGCCCCGACACCCAGACCGACCTTGACCGC
CCACCTGGCAGGAGCAGGACAGGACGGCCGGACGCGGCCATGGCCGAGCTCCCGGGGGCCCTT
TCTCTGCGGGGCCCTGCTAGGCTTCCTGTGCCTGAGTGGGCTGGCCGTGGAGGTGAAGGTAC
CCACAGAGCCGCTGAGCACGCCCCCTGGGGAAGACAGCCGAGCTGACCTGCACCTACAGCACG
TCGGTGGGAGACAGCTTCGCCCTGGAGTGGAGCTTTGTGCAGCCTGGGAAACCCATCTCTGA
GTCCCATCCAATCCTGTACTTCACCAATGGCCATCTGTATCCAAGTGGTTCTAAGTCAAAGC
GGGTCAGCCTGCTTCAGAACCCCCCACAGTGGGGGTGGCCACACTGAAACTGACTGACGTC
CACCCCTCAGATACTGGAACCTACCTCTGCCAAGTCAACAACCCACCAGATTTCTACACCAA
TGGGTTGGGGCTAATCAACCTTACTGTGCTGGTTCCCCCAGTAATCCCTTATGCAGTCAGA
GTGGACAAACCTCTGTGGGAGGCTCTACTGCACTGAGATGCAGCTCTTCCGAGGGGGCTCCT
AAGCCAGTGTACAACCTGGGTGCGTCTTGGAACTTTTCCTACACCTTCTCCTGGCAGCATGGT
TCAAGATGAGGTGTCTGGCCAGCTCATTCTACCAACCTCTCCCTGACCTCCTCGGGCACCT
ACCGCTGTGTGGCCACCAACCAGATGGGCAGTGCATCCTGTGAGCTGACCCCTCTCTGTGACC
GAACCCTCCCAAGGCCGAGTGGCCGGAGCTCTGATTGGGGTGCTCCTGGGCGTGCTGTTGCT
GTCAGTTGCTGCGTTCTGCCTGGTCAGGTTCCAGAAAGAGAGGGGGAAGAAGCCCAAGGAGA
CATATGGGGGTAGTGACCTTCGGGAGGATGCCATCGCTCCTGGGATCTCTGAGCACACTTGT
ATGAGGGCTGATTCTAGCAAGGGGTTCCCTGGAAAGACCCTCGTCTGCCAGCACCGTGACGAC
CACCAAGTCCAAGCTCCCTATGGTCGTGTGACTTCTCCCGATCCCTGAGGGCGGTGAGGGGG
AATATCAATAATTAAAGTCTGTGGGTACCCTTAAAAAAAAAAAA

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FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108760
><subunit 1 of 1, 327 aa, 1 stop
><MW: 34348, pI: 7.88, NX(S/T): 2
MAELPGPFLLCGALLGFLCLSGLAWEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFALEWS
FVQPGKPISESHPILYFTNGHLYPTGSKSKRVSLQLQNPPTVGVATLKLTDVHPSDTGTYL
CQVNNPPDFYTNGLGILNLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNWV
RLGTFPTSPSGSMVQDEVSGQLILTNLSTSSGTYRCVATNQMGASCELTLSVTEPSQG
RVAGALIGVLLGVLLLSVAAFCLVRFOKERGKKPKETYGGSDLREDAIAPGISEHTCMRA
DSSKGFLERPSSASTVTTTTSKSLPMVV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 242-260

N-glycosylation sites:

Amino acids 138-142;206-210

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 90-94

N-myristoylation sites:Amino acids 11-17;117-123;159-165;213-219;224-230;244-250;
248-254**Amidation site:**

Amino acids 270-274

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 218-229

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FIGURE 237

GGATGCAGCAGAGAGGAGCAGCTGGAAGCCGTGGCTGCGCTCTCTTCCCTCTGCTGGGCG
TCCTGTCTTCCAGGGTGTTTATATCGTCTTTTCCTTGGAGATTCGTGCAGATGCCCATG
TCCGAGGTTATGTTGGAGAAAAGATCAAGTTGAAATGCACTTTCAAGTCAACTTCAGATG
TCACTGACAAGCTTACTATAGACTGGACATATCGCCCTCCCAGCAGCAGCCACACAGTAT
CAATATTTTATTATCAGTCTTTCCAGTACCCCAACCACAGCAGGCACATTTTCGGGATCGGA
TTTCTTGGGTTGGAAATGTATACAAAGGGGATGCATCTATAAGTATAAGCAACCCTACCA
TAAAGGACAATGGGACATTCAGCTGTGCTGTGAAGAATCCCCAGATGTGCACCATAATA
TTCCCATGACAGAGCTAACAGTCACAGAAAGGGGTTTTTGGCACCATGCTTTCCTCTGTGG
CCCTTCTTCCATCCTTGTCTTTGTGCCCTCAGCCGTGGTGGTTGCTCTGCTGCTGGTGA
GAATGGGGAGGAAGGCTGCTGGGCTGAAGAAGAGGAGCAGGTCTGGCTATAAGAAGTCAT
CTATTGAGGTTTCCGATGACACTGATCAGGAGGAGGAAGAGGCGTGTATGGCGAGGCTTT
GTGTCCGTTGCGCTGAGTGCCTGGATTCACTATGAAGAGACATATTGATGAAAGTCTG
TATGACACAAGAAGAGTCACCTAAAGACAGGAAACATCCCATTCCACTGGCAGCTAAAGC
CTGTCAGAGAAAGTGGAGCTGGCCTGGACCATAGCGATGGACAATCCTGGAGATCATCAG
TAAAGACTTTAGGAACCACTTATTTATTGAATAAATGTTCTTGTGTTATTTATAAACTGT
TCAGGAAGTCTCATAAGAGACTCATGACTTCCCCTTTCAATGAATTATGCTGTAATTGAA
TGAAGAAATTCTTTTCTGAGCA

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FIGURE 238

MQQRGAAGSRGCALFPLLGVLEFFQGVYIVFSLEIRADAHVRGYVGEKIKLKCTFKSTSD
VTDKLTIDWYRPPSSSHTVSIFHYQS FQYPTTAGTFRDRISWVGNVYKGDASISISNP
TIKDNGTFSCAVKNPPDVHHNIPMTELTVTERGFGTMLSSVALLSILVFVPSAVVVAL
LVRMGRKAAGLKKRSRSGYKKSSIEVSDDTDQEEEEACMARLCVRCAECLDSYEETY

Transmembrane domain

11-30
157-177

N-glycosylation site

123-127

cAMP- and cGMP-dependent protein kinase phosphorylation site

189-193
197-201

Tyrosine kinase phosphorylation site

63-71

N-myristoylation site

5-11
8-14
124-130
153-159

Amidation site

181-185

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FIGURE 239

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCC
TCGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTCGCCTCTGTT
TGGGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAACATAAAATTGAAAGCAAGATTGAAGAGAT
GGTTGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTT
TATCAGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAAA
CTCATGATGGACGGCCACGAGGTGACCGTGGTGGACAATTTCTTCAGGGCAGGAAGAGAAACGTGGAGCACTG
GATCGGACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCTCTACATCGAGGTTGACCAGATAT
ACCATCTGGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATT
GGGACATTAAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTA
TGGAGATCCTGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCT
ACGATGAAGGCAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCAGTG
GCCAGAATCTTCAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCA
GGCGCTCCAGGGGGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCAGTACGTCAGCGATC
TAGTGAATGGCCTCGTGGCTCTCATGAACAGCAACGTCAGCAGCCCGGTCAACCTGGGGAACCCAGAAGAACAC
ACAATCCTAGAATTTGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGC
CCAGGATGACCCACAGAAAAGAAAACCAGACATCAAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCC
CGCTGGAGGAAGGTTTAAACAAAGCAATTCACACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTAC
ATCCCCAAACCAAAGCCTGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACCTCTCACTTTTAGGACAC
AAGACTACCATTGTACACTTGATGGGATGTATTTTTGGCTTTTTTTTGTGTCGTTTAAAGAAAGACTTTAACA
GGTGTGATGAAGAACAACCTGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCC
TCAAAAACTGCAGATTTTGCCCTTGCACTTTTTGAATCTCTTTTTATGTAAATAGCGTAGATGCATCTCTG
CGTATTTTCAAGTTTTTTTATCTTGCTGTGAGAGCATATGTTGTGACTGTGCTTGACAGTTTTATTACTGGTT
TCTTTGTGAAGCTGAAAAGGAACATTAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAAT
AAATGAGTCGTTATACTATGCATAAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTT
TAGGGCAGATAAAAGAATTCTGTGTGAGAGCTTTATGTTTCTCTTTAATTGAGAGTTTTTCCAAGGTCTACTT
TTGAGTTGCAAACCTTGACTTTGAAATATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTT
GCTGCGTATCTGGGGCGGGGCGAGGTTGGGGGGCACAAAGTTAACATATTCTTGTTAACCATGGTTAAATATG
CTATTTTAAATAAATATTGAACTCA

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FIGURE 240

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPL
REKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMDGHEVTVVDNFFTG
RKRNVHEHWIGHENFELINHVDVVEPLYIEVDQIYHLASPPPNMYNPIKTLKTNTIGTLNM
LGLAKRVGARLLLASTSEVYGDPEVHPQSEDIWGHVNPIGPRACYDEGKRVAETMCYAYMKQ
EGVEVRVARI FNTFGPRMHMNDGRVVS NFILQALQGEPLTVYSGSQTRAFQYVSDLVNGLV
ALMNSNVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKLML
GWEPVVPLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTSH

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41,101-107,383-389

Amidation sites:

amino acids 123-127,233-237

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FIGURE 241

GCCCGGTGGAGAATTAGGTGCTGCTGGGAGCTCCTGCCTCCCACAGGATTCCAGCTGCAGGG
AGCCTCAGGGACTCTGGGCCGCACGGAGTTGGGGGCATTCCCCAGAGAGCGTCGCC**ATGGTC**
TGCAGGGAGCAGTTATCAAAGAATCAGGTCAAGTGGGTGTTGCCGGCATTACCTGTGTGTC
TGTGGTGGTCATTGCCGCAATAGTCCTTGCCATCACCTGCGGCGGCCAGGCTGTGAGCTGG
AGGCCTGCAGCCCTGATGCCGACATGCTGGACTACCTGCTGAGCCTGGGCCAGATCAGCCGG
CGAGATGCCTTGAGAGTCACCTGGTACCACGCAGCCAACAGCAAGAAAGCCATGACAGCTGC
CCTGAACAGCAACATCACAGTCCTGGAGGCTGACGTCAATGTAGAAGGGCTCGGCACAGCCA
ATGAGACAGGAGTTCCCATCATGGCACACCCCCCACTATCTACAGTGACAACACACTGGAG
CAGTGGCTGGACGCTGTGCTGGGCTCTTCCCAAAGGGCATCAAAGTGGACTTCAAGAACAT
CAAGGCAGTGGGCCCTCCCTGGACCTCCTGCGGCAGCTGACAGAGGAAGGCAAAGTCCGGC
GGCCCATATGGATCAACGCTGACATCTTAAAGGGCCCCAACATGCTCATCTCAACTGAGGTC
AATGCCACACAGTTCCTGGCCCTGGTCCAGGAGAAGTATCCCAAGGCTACCTTATCTCCAGG
CTGGACCACCTTCTACATGTCCACGTCCCCAAACAGGACGTACACCCAAGCCATGGTGGAGA
AGATGCACGAGCTGGTGGGAGGAGTGCCCCAGAGGGTCACCTTCCCTGTACGGTCTTCCATG
GTGCGGGCTGCCTGGCCCCACTTCAGCTGGCTGCTGAGCCAATCTGAGAGGTACAGCCTGAC
GCTGTGGCAGGCTGCCTCGGACCCCCATGTGGTGGAAGATCTGCTCTACGTCCGGGATAACA
CTGCTGTCCACCAAGTCTACTATGACATCTTTGAGCCTCTCCTGTACAGTTCAAGCAGCTG
GCCTTGAATGCCACACGGAAACCAATGTACTACAGGGAGGCAGCCTGATCCCTCTTCTCCA
GCTGCCTGGGGATGACGGTCTGAATGTGGAGTGGCTGGTTCCCTGACGTCCAGGGCAGCGGTA
AAACAGCAACAATGACCCTCCCAGACACAGAAGGCATGATCCTGCTGAACACTGGCCTCGAG
GGAAGTGTGGCTGAAAACCCCGTGCCCATTTGTTCACTCCAAGTGGCAACATCCTGACGCT
GGAGTCCTGCCTGCAGCAGCTGGCCACACATCCCGGACACTGGGGCATCCATTTGCAAATAG
TGGAGCCCGCAGCCCTCCGGCCATCCCTGGCCTTGCTGGCACGCCTCTCCAGCCTTGGCCTC
TTGCATTGGCCTGTGTGGGTTGGGGCCAAATCTCCCACGGGAGTTTTTTCGGTCCCCGGCCA
TGTGGCTGGCAGAGAGCTGCTTACAGCTGTGGCTGAGGTCTTCCCCACGTGACTGTGGCAC
CAGGCTGGCCTGAGGAGGTGCTGGGCAGTGGCTACAGGGAACAGCTGCTCACAGATATGCTA
GAGTTGTGCCAGGGGCTCTGGCAACCTGTGTCTTCCAGATGCAGGCCATGCTGCTGGGCCA
CAGCACAGCTGGAGCCATAGGCAGGCTGCTGGCATCCTCCCCCGGGCCACCGTCACAGTGGAG
CACAACCCAGCTGGGGGCGACTATGCCTCTGTGAGGACAGCATTGCTGGCAGCTAGGGCTGT
GGACAGGACCCGAGTCTACTACAGGCTACCCCAGGGCTACCACAAGGACTTGCTGGCTCATG
TTGGTAGAAAT**TGAG**CACCCAGGGGTGGTGGGCCAGCGGACCTCAGGGCGGAGGCTTCCCAC
GGGGAGGCAGGAAGAAATAAAGGTCTTTGGCTTTCTCCAGGCCAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 242

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119514
><subunit 1 of 1, 585 aa, 1 stop
><MW: 64056, pI: 6.58, NX(S/T): 5
MVCREQLSKNQVKWVFAGITCVSVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG
QISRRDALEVWYHAANSKKAMTAALNSNITVLEADVNEGLGTANETGVPIMAHPTIY
SDNTLEQWLDAVLGSSQKGIKLDKFNKAVGPSLDLLRQLTEEGKVRPPIWINADILKGP
NMLISTEVNATQFLALVQEKYPKATLSPGWTTFFYMSTSPNRTYTQAMVEKMHELVGVPQ
RVTFPVRSSMVRAAWPHFSWLLSQSERYSLTWQAASDPMSVEDLLYVRDNTAVHQVYYD
IFEPLLSQFKQLALNATRKPMYYTGGSLLPQLPGDDGLNVEWLVPDVQSGSKTATMTL
PDTEGMILLNTGLEGTVAENPVPIVHTPSGNIILTLESCLOQLATHPGHWGIHLQIVEPAA
LRPSLALLARLSSLGLLHWPVWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVPAGW
PEEVLGSGYREQLLTDMLELCQGLWQPVSFQMAMLLGHSTAGAIGRLLASSPRATVTVE
HNPAGGDYASVRTALLAARAVDRTRVYYRLPQGYHKDLLAHVGRN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 18-37 (Possible type II)

N-glycosylation sites:

Amino acids 89-93;106-110;189-193;220-224;315-319

Tyrosine kinase phosphorylation site:

Amino acids 65-74

N-myristoylation sites:

Amino acids 101-107;351-357;372-378;390-396;444-450;545-551

Aminotransferases class-V pyridoxal-phosphate attachment site:

Amino acids 312-330

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FIGURE 243

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCA**ATGGC**
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTT
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACACTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATT**TGACC**AGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAC
CAAAAGGAAGATGGGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCCTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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FIGURE 244

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/17800

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/67 C12N5/10 C12N1/21 C12N1/19
C07K14/47 C07K14/705 C07K16/18 G01N33/68 G01N33/574

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, SEQUENCE SEARCH, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 6 060 249 A (BAKER KEVIN ET AL) 9 May 2000 (2000-05-09) the whole document	1-3, 5-11, 13-19, 24-26
X	KLEIN R D ET AL: "SELECTION FOR GENES ENCODING SECRETED PROTEINS AND RECEPTORS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 93, no. 14, 9 July 1996 (1996-07-09), pages 7108-7113, XP002061411 ISSN: 0027-8424 cited in the application the whole document	1-3, 5-11, 13-19, 24-26

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

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"E" earlier document but published on or after the international filing date

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"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document: member of the same patent family

Date of the actual completion of the international search

4 June 2002

Date of mailing of the international search report

11 09. 2002

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Madruga, J

INTERNATIONAL SEARCH REPORT

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/17800

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 00 55177 A (HUMAN GENOME SCIENCES INC ;ROSEN CRAIG A (US); RUBEN STEVEN M (US)) 21 September 2000 (2000-09-21) SEQ ID NO: 12 claims	1-3, 5-11, 13-19,26
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L	--- DATABASE EMBL [Online] L: Sequence information for WO 01 55315, 7 November 2001 (2001-11-07) Database accession no. AAS28811 XP002200786 SEQ ID NO: 57 abstract	1-3, 5-11, 13-19, 24-26
E	--- WO 01 54474 A (HUMAN GENOME SCIENCES INC ;ROSEN CRAIG A (US); BARASH STEVEN C (US)) 2 August 2001 (2001-08-02) SEQ ID NO: 141, SEQ ID NO: 561 claims; table 1	1-3, 5-11, 13-19, 24-26
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A	--- WO 99 54466 A (FISHER PAUL B ;HUANG FEI (US); GOLDSTEIN NEIL I (US)) 28 October 1999 (1999-10-28) the whole document -----	24,25

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/17800

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 24, 24 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see FURTHER INFORMATION sheet, invention 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1; Claims: 1-3, 5-11, 13-19,
24-26 (all partly)

A polynucleotide comprising a sequence provided in SEQ ID NO:1, a polynucleotide comprising a sequence having at least 80% identity to the polynucleotide of SEQ ID NO:1, a vector and a host containing said polynucleotides, an oligonucleotide probe derived from said nucleotide sequence, a polypeptide encoded by said polynucleotide sequence, a polypeptide having at least 80% identity to the polypeptide shown in SEQ ID NO: 2, process to produce said polypeptide, a chimeric molecule comprising said polypeptide, an antibody that specifically binds to the encoded polypeptide, a nucleic acid having at least 80% identity to the nucleotide sequence encoding the polypeptide shown in SEQ ID NO: 2, a nucleotide sequence encoding the extracellular domain of the polypeptide shown in SEQ ID NO: 2, a method to stimulate cell proliferation or differentiation, a method for detecting the presence of tumor in a mammal.

Inventions: 2-122; Claims: 1-26 (all partly,
in so far applicable)

As invention 1, the subject-matter of each invention being limited to a SEQ ID NO, wherein:

Invention 2 is limited to SEQ ID NO 3 and 4,
Invention 3 is limited to SEQ ID NO 5 and 6, etc.

...
Invention 122 is limited to SEQ ID NO 243 and 244

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/17800

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